

SEQUENCE LISTING

<110> SHIMADA, Hideaki
TOMONAGA, Takeshi
HIWASA, Takaki
MATSUSHITA, Kazuyuki
OCHIAI, Takenori
NOMURA, Fumio

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<150> JP 2004-095732

<150> 2004-03-29

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Leu Val Ser Arg Leu Thr Leu Tyr Asp Ile Ala His Thr Pro Gly Val
3/201

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55

60

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Leu Gly Pro Glu Gln Leu Pro Asp Cys Leu Lys Gly Cys Asp Val Val
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Leu Phe Asn Thr Asn Ala Thr Ile Val Ala Thr Leu Thr Ala Ala Cys
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Ala Gln His Cys Pro Glu Ala Met Ile Cys Val Ile Ala Asn Pro Val
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Tyr Asn Pro Asn Lys Ile Phe Gly Val Thr Thr Leu Asp Ile Val Arg
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Ala Asn Thr Phe Val Ala Glu Leu Lys Gly Leu Asp Pro Ala Arg Val
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Ile Ser Gln Cys Thr Pro Lys Val Asp Phe Pro Gln Asp Gln Leu Thr
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Val Glu Cys Ser Phe Val Lys Ser Gln Glu Thr Glu Cys Thr Tyr Phe
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Gln Gln Ala Asp Glu Ala Glu Asp Arg Ala Gln Gly Leu Gln Arg Glu
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5/201

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gct gca gat gag agt gag aga gga atg aag gtg ata gaa aac cgg gcc Ala Ala Asp Glu Ser Glu Arg Gly Met Lys Val Ile Glu Asn Arg Ala	85	90	95	344
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Val Ala Ala Leu Asn Arg Arg Ile Gln Leu Val Glu Glu Glu Leu Asp
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Arg Ala Gln Glu Arg Leu Ala Thr Ala Leu Gln Lys Leu Glu Glu Ala
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Arg Ala Met Lys Asp Glu Glu Lys Met Glu Ile Gln Glu Met Gln Leu
100 105 110

Lys Glu Ala Lys His Ile Ala Glu Glu Ala Asp Arg Lys Tyr Glu Glu
115 120 125

Val Ala Arg Lys Leu Val Ile Leu Glu Gly Glu Leu Glu Arg Ala Glu
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Glu Arg Ala Glu Val Ser Glu Leu Lys Cys Gly Asp Leu Glu Glu Glu
145 150 155 160

Leu Lys Asn Val Thr Asn Asn Leu Lys Ser Leu Glu Ala Ala Ser Glu
165 170 175

Lys Tyr Ser Glu Lys Glu Asp Lys Tyr Glu Glu Glu Ile Lys Leu Leu
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Ser Asp Lys Leu Lys Glu Ala Glu Thr Arg Ala Glu Phe Ala Glu Arg
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Thr Val Ala Lys Leu Glu Lys Thr Ile Asp Asp Leu Glu Glu Lys Leu
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ccagctccccg gataaacggc gcgccgcgcg gag atg aca gcc gag gag atg aag 174
Met Thr Ala Glu Glu Met Lys
1 5
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Ala Thr Glu Ser Gly Ala Gln Ser Ala Pro Leu Pro Met Glu Gly Val
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Asp Ile Ser Pro Lys Gln Asp Glu Gly Val Leu Lys Val Ile Lys Arg
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Glu Gly Thr Gly Thr Glu Met Pro Met Ile Gly Asp Arg Val Phe Val
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cac tac act ggc tgg cta tta gat ggc aca aag ttt gac tcc agt ctg 366

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Lys	Ala	Trp	Asp	Ile	Ala	Ile	Ala	Thr	Met	Lys	Val	Gly	Glu	Val	Cys	
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His	Ile	Thr	Cys	Lys	Pro	Glu	Tyr	Ala	Tyr	Gly	Ser	Ala	Gly	Ser	Pro	
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Pro	Lys	Ile	Pro	Pro	Asn	Ala	Thr	Leu	Val	Phe	Glu	Val	Glu	Leu	Phe	
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Lys	Glu	Lys	Phe	Gln	Ile	Pro	Pro	Asn	Ala	Glu	Leu	Lys	Tyr	Glu	Leu	
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Lys Lys Leu Tyr Ala Asn Met Phe Glu Arg Leu Ala Glu Glu Glu Asn	
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aag gcc aag gca gag gct tcc tca gga gac cat ccc act gac aca gag	1470
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Glu Thr Glu Ala

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Val Leu Lys Val Ile Lys Arg Glu Gly Thr Gly Thr Glu Met Pro Met
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Ile Gly Asp Arg Val Phe Val His Tyr Thr Gly Trp Leu Leu Asp Gly
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Thr Lys Phe Asp Ser Ser Leu Asp Arg Lys Asp Lys Phe Ser Phe Asp
65 70 75 80

Leu Gly Lys Gly Glu Val Ile Lys Ala Trp Asp Ile Ala Ile Ala Thr
85 90 95

Met Lys Val Gly Glu Val Cys His Ile Thr Cys Lys Pro Glu Tyr Ala
100 105 110

Tyr Gly Ser Ala Gly Ser Pro Pro Lys Ile Pro Pro Asn Ala Thr Leu
115 120 125

Val Phe Glu Val Glu Leu Phe Glu Phe Lys Gly Glu Asp Leu Thr Glu
130 135 140

Glu Glu Asp Gly Gly Ile Ile Arg Arg Ile Gln Thr Arg Gly Glu Gly
145 150 155 160

Tyr Ala Lys Pro Asn Glu Gly Ala Ile Val Glu Val Ala Leu Glu Gly
165 170 175

Tyr Tyr Lys Asp Lys Leu Phe Asp Gln Arg Glu Leu Arg Phe Glu Ile
180 185 190

Gly Glu Gly Glu Asn Leu Asp Leu Pro Tyr Gly Leu Glu Arg Ala Ile
195 200 205

Gln Arg Met Glu Lys Gly Glu His Ser Ile Val Tyr Leu Lys Pro Ser
210 215 220

Tyr Ala Phe Gly Ser Val Gly Lys Glu Lys Phe Gln Ile Pro Pro Asn
225 230 235 240

Ala Glu Leu Lys Tyr Glu Leu His Leu Lys Ser Phe Glu Lys Ala Lys
245 250 255

Glu Ser Trp Glu Met Asn Ser Glu Glu Lys Leu Glu Gln Ser Thr Ile
13/201

260	265	270
Val Lys Glu Arg Gly Thr Val Tyr Phe Lys Glu Gly Lys Tyr Lys Gln		
275	280	285
Ala Leu Leu Gln Tyr Lys Lys Ile Val Ser Trp Leu Glu Tyr Glu Ser		
290	295	300
Ser Phe Ser Asn Glu Glu Ala Gln Lys Ala Gln Ala Leu Arg Leu Ala		
305	310	315 320
Ser His Leu Asn Leu Ala Met Cys His Leu Lys Leu Gln Ala Phe Ser		
325	330	335
Ala Ala Ile Glu Ser Cys Asn Lys Ala Leu Glu Leu Asp Ser Asn Asn		
340	345	350
Glu Lys Gly Leu Phe Arg Arg Gly Glu Ala His Leu Ala Val Asn Asp		
355	360	365
Phe Glu Leu Ala Arg Ala Asp Phe Gln Lys Val Leu Gln Leu Tyr Pro		
370	375	380
Asn Asn Lys Ala Ala Lys Thr Gln Leu Ala Val Cys Gln Gln Arg Ile		
385	390	395 400
Arg Arg Gln Leu Ala Arg Glu Lys Lys Leu Tyr Ala Asn Met Phe Glu		
405	410	415
Arg Leu Ala Glu Glu Glu Asn Lys Ala Lys Ala Glu Ala Ser Ser Gly		
420	425	430
Asp His Pro Thr Asp Thr Glu Met Lys Glu Glu Gln Lys Ser Asn Thr		
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Ala Gly Ser Gln Ser Gln Val Glu Thr Glu Ala		
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 Ala Ala Val Lys Thr Leu Asn Pro Lys Ala Glu Val Ala Arg Ala Gln
5 10 15

gcg gcg ctg gcg gtc aac atc agc gca gcg cgg ggt ctg cag gac gtg 154
 Ala Ala Leu Ala Val Asn Ile Ser Ala Ala Arg Gly Leu Gln Asp Val
20 25 30

cta agg acc aac ctg ggg ccc aag ggc acc atg aag atg ctc gtt tct 202
 Leu Arg Thr Asn Leu Gly Pro Lys Gly Thr Met Lys Met Leu Val Ser
35 40 45

ggc gct gga gac atc aaa ctt act aaa gac ggc aat gtg ctg ctt cac 250
 Gly Ala Gly Asp Ile Lys Leu Thr Lys Asp Gly Asn Val Leu Leu His
50 55 60 65

gaa atg caa att caa cac cca aca gct tcc tta ata gca aag gta gca 298
 Glu Met Gln Ile Gln His Pro Thr Ala Ser Leu Ile Ala Lys Val Ala
70 75 80

aca gcc cag gat gat ata act ggt gat ggt acg act tct aat gtc cta 346
 Thr Ala Gln Asp Asp Ile Thr Gly Asp Gly Thr Thr Ser Asn Val Leu
85 90 95

atc att gga gag ctg ctg aaa cag gcg gat ctc tac att tct gaa ggc 394
 Ile Ile Gly Glu Leu Leu Lys Gln Ala Asp Leu Tyr Ile Ser Glu Gly
100 105 110

ctt cat cct aga ata atc act gaa gga ttt gaa gct gca aag gaa aag 442
 Leu His Pro Arg Ile Ile Thr Glu Gly Phe Glu Ala Ala Lys Glu Lys
115 120 125

gcc ctt cag ttt ttg gaa gaa gtc aaa gta agc aga gag atg gac agg 490
 Ala Leu Gln Phe Leu Glu Glu Val Lys Val Ser Arg Glu Met Asp Arg
15/201

130	135	140	145	
gaa aca ctt ata gat gtg gcc aga aca tct ctt cgt act aaa gtt cat				538
Glu Thr Leu Ile Asp Val Ala Arg Thr Ser Leu Arg Thr Lys Val His				
	150	155	160	
gct gaa ctt gca gat gtc tta aca gag gct gta gtg gac tcc att ttg				586
Ala Glu Leu Ala Asp Val Leu Thr Glu Ala Val Val Asp Ser Ile Leu				
	165	170	175	
gcc att aaa aag caa gat gaa cct att gat ctc ttc atg att gag atc				634
Ala Ile Lys Lys Gln Asp Glu Pro Ile Asp Leu Phe Met Ile Glu Ile				
	180	185	190	
atg gag atg aaa cat aaa tct gaa act gat aca agc tta atc aga ggg				682
Met Glu Met Lys His Lys Ser Glu Thr Asp Thr Ser Leu Ile Arg Gly				
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Leu Val Leu Asp His Gly Ala Arg His Pro Asp Met Lys Lys Arg Val				
210	215	220	225	
gag gat gca tac atc ctc act tgt aac gtg tca tta gag tat gag aaa				778
Glu Asp Ala Tyr Ile Leu Thr Cys Asn Val Ser Leu Glu Tyr Glu Lys				
	230	235	240	
aca gaa gtg aat tct ggc ttt ttt tac aag agt gca gaa gag aga gaa				826
Thr Glu Val Asn Ser Gly Phe Phe Tyr Lys Ser Ala Glu Glu Arg Glu				
	245	250	255	
aaa ctc gtg aaa gct gaa aga aaa ttc att gaa gat agg gtt aaa aaa				874
Lys Leu Val Lys Ala Glu Arg Lys Phe Ile Glu Asp Arg Val Lys Lys				
	260	265	270	
ata ata gaa ctg aaa agg aaa gtc tgt ggc gat tca gat aaa gga ttt				922
Ile Ile Glu Leu Lys Arg Lys Val Cys Gly Asp Ser Asp Lys Gly Phe				
	275	280	285	
gtt gtt att aat caa aag gga att gac ccc ttt tcc tta gat gct ctt				970
Val Val Ile Asn Gln Lys Gly Ile Asp Pro Phe Ser Leu Asp Ala Leu				
290	295	300	305	
tca aaa gaa ggc ata gtc gct ctg cgc aga gct aaa agg aga aat atg				1018
Ser Lys Glu Gly Ile Val Ala Leu Arg Arg Ala Lys Arg Arg Asn Met				
	310	315	320	
gag agg ctg act ctt gct tgt ggt ggg gta gcc ctg aat tct ttt gac				1066
Glu Arg Leu Thr Leu Ala Cys Gly Gly Val Ala Leu Asn Ser Phe Asp				
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gac cta agt cct gac tgc ttg gga cat gca gga ctt gta tat gag tat Asp Leu Ser Pro Asp Cys Leu Gly His Ala Gly Leu Val Tyr Glu Tyr 340 345 350	1114
aca ttg gga gaa gag aag ttt acc ttt att gag aaa tgt aac aac cct Thr Leu Gly Glu Glu Lys Phe Thr Phe Ile Glu Lys Cys Asn Asn Pro 355 360 365	1162
cgt tct gtc aca tta ttg atc aaa gga cca aat aag cac aca ctc act Arg Ser Val Thr Leu Leu Ile Lys Gly Pro Asn Lys His Thr Leu Thr 370 375 380 385	1210
cag atc aaa gat gca gtg agg gac ggc ttg agg gct gtc aaa aat gct Gln Ile Lys Asp Ala Val Arg Asp Gly Leu Arg Ala Val Lys Asn Ala 390 395 400	1258
att gat gat ggc tgt gtg gtt cca ggt gct ggt gcc gtg gaa gtg gca Ile Asp Asp Gly Cys Val Val Pro Gly Ala Gly Ala Val Glu Val Ala 405 410 415	1306
atg gca gaa gcc ctg att aaa cat aag ccc agt gta aag ggc agg gca Met Ala Glu Ala Leu Ile Lys His Lys Pro Ser Val Lys Gly Arg Ala 420 425 430	1354
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gtt ctt gct cag aac tct ggt ttt gac ctt cag gaa aca tta gtt aaa Val Leu Ala Gln Asn Ser Gly Phe Asp Leu Gln Glu Thr Leu Val Lys 450 455 460 465	1450
att caa gca gaa cat tca gaa tca ggt cag ctt gtg ggt gtg gac ctg Ile Gln Ala Glu His Ser Glu Ser Gly Gln Leu Val Gly Val Asp Leu 470 475 480	1498
aac aca ggt gag cca atg gtg gca gca gaa gta ggc gta tgg gat aac Asn Thr Gly Glu Pro Met Val Ala Ala Glu Val Gly Val Trp Asp Asn 485 490 495	1546
tat tgt gta aag aaa cag ctt ctt cac tcc tgc act gtg att gcc acc Tyr Cys Val Lys Lys Gln Leu Leu His Ser Cys Thr Val Ile Ala Thr 500 505 510	1594
aac att ctc ttg gtt gat gag atc atg cga gct gga atg tct tct ctg Asn Ile Leu Leu Val Asp Glu Ile Met Arg Ala Gly Met Ser Ser Leu 515 520 525	1642
aaa ggt tga attgaagctt cctctgtatc tgaatcttga agactgcaaa Lys Gly	1691

530

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gtgatcctga ggattacagc tgtggaatth ttgtccaagc ttcaaataat tttgaaagaa 1751
attttcccat atgaaaaaag gagagaacac tggcatctgt tgaaatttgg aagttctgaa 1811
attatagtat ttttaaaaat tgcactgaag tgtatacaca taaagcaggt cttttatcca 1871
gtgaacagga tgttttgctt tagcagcagt gacataaaat tccatgttag ataagcatat 1931
gttacttacc ttgttattaa atatttcttg aaaagcaaat tttaatgggt aattttatgt 1991
ggacgtatgt taaattatcc aaactaccct attgttaagc atttggtttt aaaattttta 2051
tgctaataata aatgctcaag taatttaaaa tattgaaagc atccctgttg gtataaattt 2111
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aataaatggt aagttgaaac ctcaaaaaaa a 2562

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 <213> Homo sapiens

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Gln Ala Ala Leu Ala Val Asn Ile Ser Ala Ala Arg Gly Leu Gln Asp
 20 25 30

Val Leu Arg Thr Asn Leu Gly Pro Lys Gly Thr Met Lys Met Leu Val
 35 40 45

Ser Gly Ala Gly Asp Ile Lys Leu Thr Lys Asp Gly Asn Val Leu Leu
50 55 60

His Glu Met Gln Ile Gln His Pro Thr Ala Ser Leu Ile Ala Lys Val
65 70 75 80

Ala Thr Ala Gln Asp Asp Ile Thr Gly Asp Gly Thr Thr Ser Asn Val
85 90 95

Leu Ile Ile Gly Glu Leu Leu Lys Gln Ala Asp Leu Tyr Ile Ser Glu
100 105 110

Gly Leu His Pro Arg Ile Ile Thr Glu Gly Phe Glu Ala Ala Lys Glu
115 120 125

Lys Ala Leu Gln Phe Leu Glu Glu Val Lys Val Ser Arg Glu Met Asp
130 135 140

Arg Glu Thr Leu Ile Asp Val Ala Arg Thr Ser Leu Arg Thr Lys Val
145 150 155 160

His Ala Glu Leu Ala Asp Val Leu Thr Glu Ala Val Val Asp Ser Ile
165 170 175

Leu Ala Ile Lys Lys Gln Asp Glu Pro Ile Asp Leu Phe Met Ile Glu
180 185 190

Ile Met Glu Met Lys His Lys Ser Glu Thr Asp Thr Ser Leu Ile Arg
195 200 205

Gly Leu Val Leu Asp His Gly Ala Arg His Pro Asp Met Lys Lys Arg
210 215 220

Val Glu Asp Ala Tyr Ile Leu Thr Cys Asn Val Ser Leu Glu Tyr Glu
225 230 235 240

Lys Thr Glu Val Asn Ser Gly Phe Phe Tyr Lys Ser Ala Glu Glu Arg
245 250 255

Glu Lys Leu Val Lys Ala Glu Arg Lys Phe Ile Glu Asp Arg Val Lys
260 265 270

Lys Ile Ile Glu Leu Lys Arg Lys Val Cys Gly Asp Ser Asp Lys Gly
275 280 285

Phe Val Val Ile Asn Gln Lys Gly Ile Asp Pro Phe Ser Leu Asp Ala
290 295 300

Leu Ser Lys Glu Gly Ile Val Ala Leu Arg Arg Ala Lys Arg Arg Asn
305 310 315 320

Met Glu Arg Leu Thr Leu Ala Cys Gly Gly Val Ala Leu Asn Ser Phe
325 330 335

Asp Asp Leu Ser Pro Asp Cys Leu Gly His Ala Gly Leu Val Tyr Glu
340 345 350

Tyr Thr Leu Gly Glu Glu Lys Phe Thr Phe Ile Glu Lys Cys Asn Asn
355 360 365

Pro Arg Ser Val Thr Leu Leu Ile Lys Gly Pro Asn Lys His Thr Leu
370 375 380

Thr Gln Ile Lys Asp Ala Val Arg Asp Gly Leu Arg Ala Val Lys Asn
385 390 395 400

Ala Ile Asp Asp Gly Cys Val Val Pro Gly Ala Gly Ala Val Glu Val
405 410 415

Ala Met Ala Glu Ala Leu Ile Lys His Lys Pro Ser Val Lys Gly Arg
420 425 430

Ala Gln Leu Gly Val Gln Ala Phe Ala Asp Ala Leu Leu Ile Ile Pro
435 440 445

Lys Val Leu Ala Gln Asn Ser Gly Phe Asp Leu Gln Glu Thr Leu Val
 450 455 460

Lys Ile Gln Ala Glu His Ser Glu Ser Gly Gln Leu Val Gly Val Asp
 465 470 475 480

Leu Asn Thr Gly Glu Pro Met Val Ala Ala Glu Val Gly Val Trp Asp
 485 490 495

Asn Tyr Cys Val Lys Lys Gln Leu Leu His Ser Cys Thr Val Ile Ala
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Thr Asn Ile Leu Leu Val Asp Glu Ile Met Arg Ala Gly Met Ser Ser
 515 520 525

Leu Lys Gly
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 agcgggctaa gagtagaatc gtgtcgcggc tcgagagcga gagtcacgtc ccggcgctag 180
 cccagcccga cccaggccca ccgtggtgca cgcaaaccac ttcctggcc atg cgc tcc 238
 Met Arg Ser
 1

ctc ctg ctt ctc agc gcc ttc tgc ctc ctg gag gcg gcc ctg gcc gcc 286
 Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala Leu Ala Ala
 5 10 15

gag gtg aag aaa cct gca gcc gca gca gct cct ggc act gcg gag aag	334
Glu Val Lys Lys Pro Ala Ala Ala Ala Pro Gly Thr Ala Glu Lys	
20 25 30 35	
ttg agc ccc aag gcg gcc acg ctt gcc gag cgc agc gcc ggc ctg gcc	382
Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Ser Ala Gly Leu Ala	
40 45 50	
ttc agc ttg tac cag gcc atg gcc aag gac cag gca gtg gag aac atc	430
Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val Glu Asn Ile	
55 60 65	
ctg gtg tca ccc gtg gtg gtg gcc tcg tcg cta ggg ctc gtg tcg ctg	478
Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu Val Ser Leu	
70 75 80	
ggc ggc aag gcg acc acg gcg tcg cag gcc aag gca gtg ctg agc gcc	526
Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val Leu Ser Ala	
85 90 95	
gag cag ctg cgc gac gag gag gtg cac gcc ggc ctg ggc gag ctg ctg	574
Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly Glu Leu Leu	
100 105 110 115	
cgc tca ctc agc aac tcc acg gcg cgc aac gtg acc tgg aag ctg ggc	622
Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp Lys Leu Gly	
120 125 130	
agc cga ctg tac gga ccc agc tca gtg agc ttc gct gat gac ttc gtg	670
Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp Asp Phe Val	
135 140 145	
cgc agc agc aag cag cac tac aac tgc gag cac tcc aag atc aac ttc	718
Arg Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys Ile Asn Phe	
150 155 160	
cgc gac aag cgc agc gcg ctg cag tcc atc aac gag tgg gcc gcg cag	766
Arg Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp Ala Ala Gln	
165 170 175	
acc acc gac ggc aag ctg ccc gag gtc acc aag gac gtg gag cgc acg	814
Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val Glu Arg Thr	
180 185 190 195	
gac ggc gcc ctg cta gtc aac gcc atg ttc ttc aag cca cac tgg gat	862
Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro His Trp Asp	
200 205 210	
gag aaa ttc cac cac aag atg gtg gac aac cgt ggc ttc atg gtg act	910

Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe Met Val Thr	
215 220 225	
cgg tcc tat acc gtg ggt gtc atg atg atg cac cgg aca ggc ctc tac	958
Arg Ser Tyr Thr Val Gly Val Met Met Met His Arg Thr Gly Leu Tyr	
230 235 240	
aac tac tac gac gac gag aag gaa aag ctg caa atc gtg gag atg ccc	1006
Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Ile Val Glu Met Pro	
245 250 255	
ctg gcc cac aag ctc tcc agc ctc atc atc ctc atg ccc cat cac gtg	1054
Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro His His Val	
260 265 270 275	
gag cct ctc gag cgc ctt gaa aag ctg cta acc aaa gag cag ctg aag	1102
Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu Gln Leu Lys	
280 285 290	
atc tgg atg ggg aag atg cag aag aag gct gtt gcc atc tcc ttg ccc	1150
Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile Ser Leu Pro	
295 300 305	
aag ggt gtg gtg gag gtg acc cat gac ctg cag aaa cac ctg gct ggg	1198
Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His Leu Ala Gly	
310 315 320	
ctg ggc ctg act gag gcc att gac aag aac aag gcc gac ttg tca cgc	1246
Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp Leu Ser Arg	
325 330 335	
atg tca ggc aag aag gac ctg tac ctg gcc agc gtg ttc cac gcc acc	1294
Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe His Ala Thr	
340 345 350 355	
gcc ttt gag ttg gac aca gat ggc aac ccc ttt gac cag gac atc tac	1342
Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln Asp Ile Tyr	
360 365 370	
ggg cgc gag gag ctg cgc agc ccc aag ctg ttc tac gcc gac cac ccc	1390
Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala Asp His Pro	
375 380 385	
ttc atc ttc cta gtg cgg gac acc caa agc ggc tcc ctg cta ttc att	1438
Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu Leu Phe Ile	
390 395 400	
ggg cgc ctg gtc cgg cct aag ggt gac aag atg cga gac gag tta tag	1486
Gly Arg Leu Val Arg Pro Lys Gly Asp Lys Met Arg Asp Glu Leu	
405 410 415	

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aa 2208

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<212> PRT
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Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Ala Pro Gly Thr
20           25           30

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Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Ser Ala
35           40           45

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Gly Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val
50           55           60

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Glu Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu
65 70 75 80

Val Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val
85 90 95

Leu Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly
100 105 110

Glu Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp
115 120 125

Lys Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp
130 135 140

Asp Phe Val Arg Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys
145 150 155 160

Ile Asn Phe Arg Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp
165 170 175

Ala Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val
180 185 190

Glu Arg Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro
195 200 205

His Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe
210 215 220

Met Val Thr Arg Ser Tyr Thr Val Gly Val Met Met Met His Arg Thr
225 230 235 240

Gly Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Ile Val
245 250 255

Glu Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro
25/201

260

265

270

His His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu
 275 280 285

Gln Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile
 290 295 300

Ser Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His
 305 310 315 320

Leu Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp
 325 330 335

Leu Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe
 340 345 350

His Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln
 355 360 365

Asp Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala
 370 375 380

Asp His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu
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 405 410 415

Glu Leu

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<222> (77).. (1429)

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Met Val Pro Leu Val Ala Val Val Ser Gly Pro Arg
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gcc cag ctc ttt gcc tgc ctg ctc agg ctg ggc act cag cag gtc ggc 160
Ala Gln Leu Phe Ala Cys Leu Leu Arg Leu Gly Thr Gln Gln Val Gly
15 20 25

ccc ctt cag ctg cac acc ggg gcc agc cat gcg gcc agg aac cat tat 208
Pro Leu Gln Leu His Thr Gly Ala Ser His Ala Ala Arg Asn His Tyr
30 35 40

gag gtg ctg gtg ctg ggt ggg ggc agt ggc gga atc acc atg gct gcc 256
Glu Val Leu Val Leu Gly Gly Gly Ser Gly Gly Ile Thr Met Ala Ala
45 50 55 60

cgc atg aag agg aaa gtg ggt gca gag aat gtg gcc att gtt gag ccc 304
Arg Met Lys Arg Lys Val Gly Ala Glu Asn Val Ala Ile Val Glu Pro
65 70 75

agt gag aga cat ttc tac cag cca atc tgg aca ctg gtg ggt gct ggt 352
Ser Glu Arg His Phe Tyr Gln Pro Ile Trp Thr Leu Val Gly Ala Gly
80 85 90

gcc aaa caa ttg tcc tca tct ggt cgt ccc acg gca agt gtg att cca 400
Ala Lys Gln Leu Ser Ser Ser Gly Arg Pro Thr Ala Ser Val Ile Pro
95 100 105

tct ggt gta gaa tgg atc aaa gct aga gtg act gag ttg aac cca gac 448
Ser Gly Val Glu Trp Ile Lys Ala Arg Val Thr Glu Leu Asn Pro Asp
110 115 120

aag aac tgc att cac aca gat gac gac gag aag atc tcc tac cga tat 496
Lys Asn Cys Ile His Thr Asp Asp Asp Glu Lys Ile Ser Tyr Arg Tyr
125 130 135 140

ctt att att gct ctc gga atc cag ctg gac tat gag aag att aaa ggc 544
Leu Ile Ile Ala Leu Gly Ile Gln Leu Asp Tyr Glu Lys Ile Lys Gly
145 150 155

cta cct gaa ggt ttc gct cat ccc aaa ata ggg tcg aat tat tca gtt 592
Leu Pro Glu Gly Phe Ala His Pro Lys Ile Gly Ser Asn Tyr Ser Val
160 165 170

aag act gta gag aag aca tgg aaa gct ctg cag gac ttc aaa gag ggc Lys Thr Val Glu Lys Thr Trp Lys Ala Leu Gln Asp Phe Lys Glu Gly 175 180 185	640
aat gcc atc ttc acc ttc cca aat act cca gtg aag tgt gct gga gcc Asn Ala Ile Phe Thr Phe Pro Asn Thr Pro Val Lys Cys Ala Gly Ala 190 195 200	688
cct cag aag atc atg tac tta tca gaa gcc tac ttc agg aag aca ggg Pro Gln Lys Ile Met Tyr Leu Ser Glu Ala Tyr Phe Arg Lys Thr Gly 205 210 215 220	736
aag cga tcc aag gcc aat atc att ttc aac act tct ctt gga gcc att Lys Arg Ser Lys Ala Asn Ile Ile Phe Asn Thr Ser Leu Gly Ala Ile 225 230 235	784
ttc ggg gtt aag aag tat gca gat gcc ctg cag gag atc atc cag gag Phe Gly Val Lys Lys Tyr Ala Asp Ala Leu Gln Glu Ile Ile Gln Glu 240 245 250	832
cgg aac ctc act gtt aac tac aag aaa aac ctc att gaa gtc cga gcc Arg Asn Leu Thr Val Asn Tyr Lys Lys Asn Leu Ile Glu Val Arg Ala 255 260 265	880
gat aaa caa gag gct gta ttt gag aac ctg gac aaa cca gga gag acc Asp Lys Gln Glu Ala Val Phe Glu Asn Leu Asp Lys Pro Gly Glu Thr 270 275 280	928
caa gtg att tca tat gaa atg ctt cat gtc aca cct cca atg agc cca Gln Val Ile Ser Tyr Glu Met Leu His Val Thr Pro Pro Met Ser Pro 285 290 295 300	976
cca gat gtc ctc aag acc agt cct gtg gct gat gct gct ggt tgg gtg Pro Asp Val Leu Lys Thr Ser Pro Val Ala Asp Ala Ala Gly Trp Val 305 310 315	1024
gat gtg gat aaa gaa act ctg caa cac agg agg tac cca aat gtg ttt Asp Val Asp Lys Glu Thr Leu Gln His Arg Arg Tyr Pro Asn Val Phe 320 325 330	1072
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Lys Val Gly Ala Glu Asn Val Ala Ile Val Glu Pro Ser Glu Arg His
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Ser Ser Ser Gly Arg Pro Thr Ala Ser Val Ile Pro Ser Gly Val Glu
100 105 110

Trp Ile Lys Ala Arg Val Thr Glu Leu Asn Pro Asp Lys Asn Cys Ile
115 120 125

His Thr Asp Asp Asp Glu Lys Ile Ser Tyr Arg Tyr Leu Ile Ile Ala
130 135 140

Leu Gly Ile Gln Leu Asp Tyr Glu Lys Ile Lys Gly Leu Pro Glu Gly
145 150 155 160

Phe Ala His Pro Lys Ile Gly Ser Asn Tyr Ser Val Lys Thr Val Glu
165 170 175

Lys Thr Trp Lys Ala Leu Gln Asp Phe Lys Glu Gly Asn Ala Ile Phe
180 185 190

Thr Phe Pro Asn Thr Pro Val Lys Cys Ala Gly Ala Pro Gln Lys Ile
195 200 205

Met Tyr Leu Ser Glu Ala Tyr Phe Arg Lys Thr Gly Lys Arg Ser Lys
210 215 220

Ala Asn Ile Ile Phe Asn Thr Ser Leu Gly Ala Ile Phe Gly Val Lys
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Lys Tyr Ala Asp Ala Leu Gln Glu Ile Ile Gln Glu Arg Asn Leu Thr
245 250 255

Val Asn Tyr Lys Lys Asn Leu Ile Glu Val Arg Ala Asp Lys Gln Glu
260 265 270

Ala Val Phe Glu Asn Leu Asp Lys Pro Gly Glu Thr Gln Val Ile Ser
275 280 285

Tyr Glu Met Leu His Val Thr Pro Pro Met Ser Pro Pro Asp Val Leu
290 295 300

Lys Thr Ser Pro Val Ala Asp Ala Ala Gly Trp Val Asp Val Asp Lys
305 310 315 320

Glu Thr Leu Gln His Arg Arg Tyr Pro Asn Val Phe Gly Ile Gly Asp
325 330 335

Cys Thr Asn Leu Pro Thr Ser Lys Thr Ala Ala Ala Val Ala Ala Gln
340 345 350

Ser Gly Ile Leu Asp Arg Thr Ile Ser Val Ile Met Lys Asn Gln Thr
355 360 365

Pro Thr Lys Lys Tyr Asp Gly Tyr Thr Ser Cys Pro Leu Val Thr Gly
370 375 380

Tyr Asn Arg Val Ile Leu Ala Glu Phe Asp Tyr Lys Ala Glu Pro Leu
385 390 395 400

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405 410 415

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Pro Leu Arg Phe Asp Gly Arg Val Val Leu Val Thr Gly Ala Gly Ala
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gga ttg ggc cga gcc tat gcc ctg gct ttt gca gaa aga gga gcg tta 153
Gly Leu Gly Arg Ala Tyr Ala Leu Ala Phe Ala Glu Arg Gly Ala Leu
20 25 30 35

gtt gtt gtg aat gat ttg gga ggg gac ttc aaa gga gtt ggt aaa ggc 201
Val Val Val Asn Asp Leu Gly Gly Asp Phe Lys Gly Val Gly Lys Gly
40 45 50

tcc tta gct gct gat aag gtt gtt gaa gaa ata aga agg aga ggt gga 249
Ser Leu Ala Ala Asp Lys Val Val Glu Glu Ile Arg Arg Arg Gly Gly
55 60 65

aaa gca gtg gcc aac tat gat tca gtg gaa gaa gga gag aag gtt gtg 297
Lys Ala Val Ala Asn Tyr Asp Ser Val Glu Glu Gly Glu Lys Val Val
70 75 80

aag aca gcc ctg gat gct ttt gga aga ata gat gtt gtg gtc aac aat 345
Lys Thr Ala Leu Asp Ala Phe Gly Arg Ile Asp Val Val Val Asn Asn
85 90 95

gct gga att ctg agg gat cgt tcc ttt gct agg ata agt gat gaa gac 393
Ala Gly Ile Leu Arg Asp Arg Ser Phe Ala Arg Ile Ser Asp Glu Asp
100 105 110 115

tgg gat ata atc cac aga gtt cat ttg cgg ggt tca ttc caa gtg aca 441
Trp Asp Ile Ile His Arg Val His Leu Arg Gly Ser Phe Gln Val Thr
120 125 130

cgg gca gca tgg gaa cac atg aag aaa cag aag tat gga agg att att	489
Arg Ala Ala Trp Glu His Met Lys Lys Gln Lys Tyr Gly Arg Ile Ile	
135 140 145	
atg act tca tca gct tca gga ata tat ggc aac ttt ggc cag gcc aat	537
Met Thr Ser Ser Ala Ser Gly Ile Tyr Gly Asn Phe Gly Gln Ala Asn	
150 155 160	
tat agt gct gca aag ttg ggt ctt ctg ggc ctt gca aat tct ctt gca	585
Tyr Ser Ala Ala Lys Leu Gly Leu Leu Gly Leu Ala Asn Ser Leu Ala	
165 170 175	
att gaa ggc agg aaa agc aac att cat tgt aac acc att gct cct aat	633
Ile Glu Gly Arg Lys Ser Asn Ile His Cys Asn Thr Ile Ala Pro Asn	
180 185 190 195	
gcg gga tca cgg atg act cag aca gtt atg cct gaa gat ctt gtg gaa	681
Ala Gly Ser Arg Met Thr Gln Thr Val Met Pro Glu Asp Leu Val Glu	
200 205 210	
gcc ctg aag cca gag tat gtg gca cct ctt gtc ctt tgg ctt tgt cac	729
Ala Leu Lys Pro Glu Tyr Val Ala Pro Leu Val Leu Trp Leu Cys His	
215 220 225	
gag agt tgt gag gag aat ggt ggc ttg ttt gag gtt gga gca gga tgg	777
Glu Ser Cys Glu Glu Asn Gly Gly Leu Phe Glu Val Gly Ala Gly Trp	
230 235 240	
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Ile Gly Lys Leu Arg Trp Glu Arg Thr Leu Gly Ala Ile Val Arg Gln	
245 250 255	
aag aat cac cca atg act cct gag gca gtc aag gct aac tgg aag aag	873
Lys Asn His Pro Met Thr Pro Glu Ala Val Lys Ala Asn Trp Lys Lys	
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atc tgt gac ttt gag aat gcc agc aag cct cag agt atc caa gaa tca	921
Ile Cys Asp Phe Glu Asn Ala Ser Lys Pro Gln Ser Ile Gln Glu Ser	
280 285 290	
act ggc agt ata att gaa gtt ctg agt aaa ata gat tca gaa gga gga	969
Thr Gly Ser Ile Ile Glu Val Leu Ser Lys Ile Asp Ser Glu Gly Gly	
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Val Ser Ala Asn His Thr Ser Arg Ala Thr Ser Thr Ala Thr Ser Gly	
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ttt gct gga gct att ggc cag aaa ctc cct cca ttt tct tat gct tat	1065

Phe	Ala	Gly	Ala	Ile	Gly	Gln	Lys	Leu	Pro	Pro	Phe	Ser	Tyr	Ala	Tyr		
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Thr	Glu	Leu	Glu	Ala	Ile	Met	Tyr	Ala	Leu	Gly	Val	Gly	Ala	Ser	Ile		
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aag	gat	cca	aaa	gat	ttg	aaa	ttt	att	tat	gaa	gga	agt	tct	gat	ttc	1161	
Lys	Asp	Pro	Lys	Asp	Leu	Lys	Phe	Ile	Tyr	Glu	Gly	Ser	Ser	Asp	Phe		
				360					365						370		
tcc	tgt	ttg	ccc	acc	ttc	gga	gtt	atc	ata	ggt	cag	aaa	tct	atg	atg	1209	
Ser	Cys	Leu	Pro	Thr	Phe	Gly	Val	Ile	Ile	Gly	Gln	Lys	Ser	Met	Met		
			375						380						385		
ggt	gga	gga	tta	gca	gaa	att	cct	gga	ctt	tca	atc	aac	ttt	gca	aag	1257	
Gly	Gly	Gly	Leu	Ala	Glu	Ile	Pro	Gly	Leu	Ser	Ile	Asn	Phe	Ala	Lys		
			390					395					400				
gtt	ctt	cat	gga	gag	cag	tac	tta	gag	tta	tat	aaa	cca	ctt	ccc	aga	1305	
Val	Leu	His	Gly	Glu	Gln	Tyr	Leu	Glu	Leu	Tyr	Lys	Pro	Leu	Pro	Arg		
	405					410						415					
gca	gga	aaa	tta	aaa	tgt	gaa	gca	gtt	gtt	gct	gat	gtc	cta	gat	aaa	1353	
Ala	Gly	Lys	Leu	Lys	Cys	Glu	Ala	Val	Val	Ala	Asp	Val	Leu	Asp	Lys		
420					425					430					435		
gga	tcc	ggt	gta	gtg	att	att	atg	gat	gtc	tat	tct	tat	tct	gag	aag	1401	
Gly	Ser	Gly	Val	Val	Ile	Ile	Met	Asp	Val	Tyr	Ser	Tyr	Ser	Glu	Lys		
				440					445						450		
gaa	ctt	ata	tgc	cac	aat	cag	ttc	tct	ctc	ttt	ctt	gtt	ggc	tct	gga	1449	
Glu	Leu	Ile	Cys	His	Asn	Gln	Phe	Ser	Leu	Phe	Leu	Val	Gly	Ser	Gly		
			455						460						465		
ggc	ttt	ggt	gga	aaa	cgg	aca	tca	gac	aaa	gtc	aag	gta	gct	gta	gcc	1497	
Gly	Phe	Gly	Gly	Lys	Arg	Thr	Ser	Asp	Lys	Val	Lys	Val	Ala	Val	Ala		
			470					475							480		
ata	cct	aat	aga	cct	cct	gat	gct	gta	ctt	aca	gat	acc	acc	tct	ctt	1545	
Ile	Pro	Asn	Arg	Pro	Pro	Asp	Ala	Val	Leu	Thr	Asp	Thr	Thr	Ser	Leu		
				485				490							495		
aat	cag	gct	gct	ttg	tac	cgc	ctc	agt	gga	gac	tgg	aat	ccc	tta	cac	1593	
Asn	Gln	Ala	Ala	Leu	Tyr	Arg	Leu	Ser	Gly	Asp	Trp	Asn	Pro	Leu	His		
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att	gat	cct	aac	ttt	gct	agt	cta	gca	ggt	ttt	gac	aag	ccc	ata	tta	1641	
Ile	Asp	Pro	Asn	Phe	Ala	Ser	Leu	Ala	Gly	Phe	Asp	Lys	Pro	Ile	Leu		
				520					525						530		

cat gga tta tgt aca ttt gga ttt tct gcc agg cgt gtg tta cag cag	1689
His Gly Leu Cys Thr Phe Gly Phe Ser Ala Arg Arg Val Leu Gln Gln	
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ttt gca gat aat gat gtg tca aga ttc aag gca att aag gct cgt ttt	1737
Phe Ala Asp Asn Asp Val Ser Arg Phe Lys Ala Ile Lys Ala Arg Phe	
550 555 560	
gca aaa cca gta tat cca gga caa act cta caa act gag atg tgg aag	1785
Ala Lys Pro Val Tyr Pro Gly Gln Thr Leu Gln Thr Glu Met Trp Lys	
565 570 575	
gaa gga aac aga att cat ttt caa acc aag gtc caa gaa act gga gac	1833
Glu Gly Asn Arg Ile His Phe Gln Thr Lys Val Gln Glu Thr Gly Asp	
580 585 590 595	
att gtc att tca aat gca tat gtg gat ctt gca cca aca tct ggt act	1881
Ile Val Ile Ser Asn Ala Tyr Val Asp Leu Ala Pro Thr Ser Gly Thr	
600 605 610	
tca gct aag aca ccc tct gag ggc ggg aag ctt cag agt acc ttt gta	1929
Ser Ala Lys Thr Pro Ser Glu Gly Gly Lys Leu Gln Ser Thr Phe Val	
615 620 625	
ttt gag gaa ata gga cgc cgc cta aag gat att ggg cct gag gtg gtg	1977
Phe Glu Glu Ile Gly Arg Arg Leu Lys Asp Ile Gly Pro Glu Val Val	
630 635 640	
aag aaa gta aat gct gta ttt gag tgg cat ata acc aaa ggc gga aat	2025
Lys Lys Val Asn Ala Val Phe Glu Trp His Ile Thr Lys Gly Gly Asn	
645 650 655	
att ggg gct aag tgg act att gac ctg aaa agt ggt tct gga aaa gtg	2073
Ile Gly Ala Lys Trp Thr Ile Asp Leu Lys Ser Gly Ser Gly Lys Val	
660 665 670 675	
tac caa ggc cct gca aaa ggt gct gct gat aca aca atc ata ctt tca	2121
Tyr Gln Gly Pro Ala Lys Gly Ala Ala Asp Thr Thr Ile Ile Leu Ser	
680 685 690	
gat gaa gat ttc atg gag gtg gtc ctg ggc aag ctt gac cct cag aag	2169
Asp Glu Asp Phe Met Glu Val Val Leu Gly Lys Leu Asp Pro Gln Lys	
695 700 705	
gca ttc ttt agt ggc agg ctg aag gcc aga ggg aac atc atg ctg agc	2217
Ala Phe Phe Ser Gly Arg Leu Lys Ala Arg Gly Asn Ile Met Leu Ser	
710 715 720	
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Gln Lys Leu Gln Met Ile Leu Lys Asp Tyr Ala Lys Leu
 725 730 735

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 cttgattatt ctgcaaaagt gattagaact aagatgcagg ggaaattgct taacattttc 2379
 agatatcaga taactgcaga ttttcatttt ctactaattt tcatgtatca ttattttttac 2439
 aaggaactat atataagcta gcacatgatt atccttctgt tcttagatct gtatcttcat 2499
 aataaaaaat ttgcccgaag tcctgtttcc ttagaatttg tgatagcatt gataagttga 2559
 aaggaaaatt aaatcaataa aggcctttga tacc 2593

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Gly Ala Leu Val Val Val Asn Asp Leu Gly Gly Asp Phe Lys Gly Val
 35 40 45

Gly Lys Gly Ser Leu Ala Ala Asp Lys Val Val Glu Glu Ile Arg Arg
 50 55 60

Arg Gly Gly Lys Ala Val Ala Asn Tyr Asp Ser Val Glu Glu Gly Glu
 65 70 75 80

Lys Val Val Lys Thr Ala Leu Asp Ala Phe Gly Arg Ile Asp Val Val
 85 90 95

Val Asn Asn Ala Gly Ile Leu Arg Asp Arg Ser Phe Ala Arg Ile Ser
 100 105 110

Asp Glu Asp Trp Asp Ile Ile His Arg Val His Leu Arg Gly Ser Phe
115 120 125

Gln Val Thr Arg Ala Ala Trp Glu His Met Lys Lys Gln Lys Tyr Gly
130 135 140

Arg Ile Ile Met Thr Ser Ser Ala Ser Gly Ile Tyr Gly Asn Phe Gly
145 150 155 160

Gln Ala Asn Tyr Ser Ala Ala Lys Leu Gly Leu Leu Gly Leu Ala Asn
165 170 175

Ser Leu Ala Ile Glu Gly Arg Lys Ser Asn Ile His Cys Asn Thr Ile
180 185 190

Ala Pro Asn Ala Gly Ser Arg Met Thr Gln Thr Val Met Pro Glu Asp
195 200 205

Leu Val Glu Ala Leu Lys Pro Glu Tyr Val Ala Pro Leu Val Leu Trp
210 215 220

Leu Cys His Glu Ser Cys Glu Glu Asn Gly Gly Leu Phe Glu Val Gly
225 230 235 240

Ala Gly Trp Ile Gly Lys Leu Arg Trp Glu Arg Thr Leu Gly Ala Ile
245 250 255

Val Arg Gln Lys Asn His Pro Met Thr Pro Glu Ala Val Lys Ala Asn
260 265 270

Trp Lys Lys Ile Cys Asp Phe Glu Asn Ala Ser Lys Pro Gln Ser Ile
275 280 285

Gln Glu Ser Thr Gly Ser Ile Ile Glu Val Leu Ser Lys Ile Asp Ser
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Glu Gly Gly Val Ser Ala Asn His Thr Ser Arg Ala Thr Ser Thr Ala
37/201

305 310 315 320

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325 330 335

Tyr Ala Tyr Thr Glu Leu Glu Ala Ile Met Tyr Ala Leu Gly Val Gly
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Ala Ser Ile Lys Asp Pro Lys Asp Leu Lys Phe Ile Tyr Glu Gly Ser
355 360 365

Ser Asp Phe Ser Cys Leu Pro Thr Phe Gly Val Ile Ile Gly Gln Lys
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Ser Met Met Gly Gly Gly Leu Ala Glu Ile Pro Gly Leu Ser Ile Asn
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Phe Ala Lys Val Leu His Gly Glu Gln Tyr Leu Glu Leu Tyr Lys Pro
405 410 415

Leu Pro Arg Ala Gly Lys Leu Lys Cys Glu Ala Val Val Ala Asp Val
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Leu Asp Lys Gly Ser Gly Val Val Ile Ile Met Asp Val Tyr Ser Tyr
435 440 445

Ser Glu Lys Glu Leu Ile Cys His Asn Gln Phe Ser Leu Phe Leu Val
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Gly Ser Gly Gly Phe Gly Gly Lys Arg Thr Ser Asp Lys Val Lys Val
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Ala Val Ala Ile Pro Asn Arg Pro Pro Asp Ala Val Leu Thr Asp Thr
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Thr Ser Leu Asn Gln Ala Ala Leu Tyr Arg Leu Ser Gly Asp Trp Asn
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Pro Leu His Ile Asp Pro Asn Phe Ala Ser Leu Ala Gly Phe Asp Lys
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Pro Ile Leu His Gly Leu Cys Thr Phe Gly Phe Ser Ala Arg Arg Val
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Ala Arg Phe Ala Lys Pro Val Tyr Pro Gly Gln Thr Leu Gln Thr Glu
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Thr Gly Asp Ile Val Ile Ser Asn Ala Tyr Val Asp Leu Ala Pro Thr
595 600 605

Ser Gly Thr Ser Ala Lys Thr Pro Ser Glu Gly Gly Lys Leu Gln Ser
610 615 620

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625 630 635 640

Glu Val Val Lys Lys Val Asn Ala Val Phe Glu Trp His Ile Thr Lys
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Gly Gly Asn Ile Gly Ala Lys Trp Thr Ile Asp Leu Lys Ser Gly Ser
660 665 670

Gly Lys Val Tyr Gln Gly Pro Ala Lys Gly Ala Ala Asp Thr Thr Ile
675 680 685

Ile Leu Ser Asp Glu Asp Phe Met Glu Val Val Leu Gly Lys Leu Asp
690 695 700

Pro Gln Lys Ala Phe Phe Ser Gly Arg Leu Lys Ala Arg Gly Asn Ile
39/201

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Met Glu Gln Val Asn Glu Leu Lys Glu Lys Gly Asn Lys Ala Leu
1 5 10 15

agc gtg ggt aac atc gat gat gcc tta cag tgc tac tcc gaa gct att 155
Ser Val Gly Asn Ile Asp Asp Ala Leu Gln Cys Tyr Ser Glu Ala Ile
20 25 30

aag ctg gat ccc cac aac cac gtg ctg tac agc aac cgt tct gct gcc 203
Lys Leu Asp Pro His Asn His Val Leu Tyr Ser Asn Arg Ser Ala Ala
35 40 45

tat gcc aag aaa gga gac tac cag aag gct tat gag gat ggc tgc aag 251
Tyr Ala Lys Lys Gly Asp Tyr Gln Lys Ala Tyr Glu Asp Gly Cys Lys
50 55 60

act gtc gac cta aag cct gac tgg ggc aag ggc tat tca cga aaa gca 299
Thr Val Asp Leu Lys Pro Asp Trp Gly Lys Gly Tyr Ser Arg Lys Ala
65 70 75

gca gct cta gag ttc tta aac cgc ttt gaa gaa gcc aag cga acc tat 347
Ala Ala Leu Glu Phe Leu Asn Arg Phe Glu Glu Ala Lys Arg Thr Tyr
80 85 90 95

gag gag ggc tta aaa cac gag gca aat aac cct caa ctg aaa gag ggt 395
Glu Glu Gly Leu Lys His Glu Ala Asn Asn Pro Gln Leu Lys Glu Gly
100 105 110

tta cag aat atg gag gcc agg ttg gca gag aga aaa ttc atg aac cct 443
Leu Gln Asn Met Glu Ala Arg Leu Ala Glu Arg Lys Phe Met Asn Pro

115	120	125	
ttc aac atg cct aat ctg tat cag aag ttg gag agt gat ccc agg aca			491
Phe Asn Met Pro Asn Leu Tyr Gln Lys Leu Glu Ser Asp Pro Arg Thr			
130	135	140	
agg aca cta ctc agt gat cct acc tac cgg gag ctg ata gag cag cta			539
Arg Thr Leu Leu Ser Asp Pro Thr Tyr Arg Glu Leu Ile Glu Gln Leu			
145	150	155	
cga aac aag cct tct gac ctg ggc acg aaa cta caa gat ccc cgg atc			587
Arg Asn Lys Pro Ser Asp Leu Gly Thr Lys Leu Gln Asp Pro Arg Ile			
160	165	170	175
atg acc act ctc agc gtc ctc ctt ggg gtc gat ctg ggc agt atg gat			635
Met Thr Thr Leu Ser Val Leu Leu Gly Val Asp Leu Gly Ser Met Asp			
180	185	190	
gag gag gaa gag att gca aca cct cca cca cca ccc cct ccc aaa aag			683
Glu Glu Glu Glu Ile Ala Thr Pro Pro Pro Pro Pro Pro Lys Lys			
195	200	205	
gag acc aag cca gag cca atg gaa gaa gat ctt cca gag aat aag aag			731
Glu Thr Lys Pro Glu Pro Met Glu Glu Asp Leu Pro Glu Asn Lys Lys			
210	215	220	
cag gca ctg aaa gaa aaa gag ctg ggg aac gat gcc tac aag aag aaa			779
Gln Ala Leu Lys Glu Lys Glu Leu Gly Asn Asp Ala Tyr Lys Lys Lys			
225	230	235	
gac ttt gac aca gcc ttg aag cat tac gac aaa gcc aag gag ctg gac			827
Asp Phe Asp Thr Ala Leu Lys His Tyr Asp Lys Ala Lys Glu Leu Asp			
240	245	250	255
ccc act aac atg act tac att acc aat caa gca gcg gta tac ttt gaa			875
Pro Thr Asn Met Thr Tyr Ile Thr Asn Gln Ala Ala Val Tyr Phe Glu			
260	265	270	
aag ggc gac tac aat aag tgc cgg gag ctt tgt gag aag gcc att gaa			923
Lys Gly Asp Tyr Asn Lys Cys Arg Glu Leu Cys Glu Lys Ala Ile Glu			
275	280	285	
gtg ggg aga gaa aac cga gaa gac tat cga cag att gcc aaa gca tat			971
Val Gly Arg Glu Asn Arg Glu Asp Tyr Arg Gln Ile Ala Lys Ala Tyr			
290	295	300	
gct cga att ggc aac tcc tac ttc aaa gaa gaa aag tac aag gat gcc			1019
Ala Arg Ile Gly Asn Ser Tyr Phe Lys Glu Glu Lys Tyr Lys Asp Ala			
305	310	315	

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ctc aag aaa tgc cag cag gca gag aaa atc ctg aag gag caa gag cgg Leu Lys Lys Cys Gln Gln Ala Glu Lys Ile Leu Lys Glu Gln Glu Arg 340 345 350	1115
ctg gcc tac ata aac ccc gac ctg gct ttg gag gag aag aac aaa ggc Leu Ala Tyr Ile Asn Pro Asp Leu Ala Leu Glu Glu Lys Asn Lys Gly 355 360 365	1163
aac gag tgt ttt cag aaa ggg gac tat ccc cag gcc atg aag cat tat Asn Glu Cys Phe Gln Lys Gly Asp Tyr Pro Gln Ala Met Lys His Tyr 370 375 380	1211
aca gaa gcc atc aaa agg aac ccg aaa gat gcc aaa tta tac agc aat Thr Glu Ala Ile Lys Arg Asn Pro Lys Asp Ala Lys Leu Tyr Ser Asn 385 390 395	1259
cga gct gcc tgc tac acc aaa ctc ctg gag ttc cag ctg gca ctc aag Arg Ala Ala Cys Tyr Thr Lys Leu Leu Glu Phe Gln Leu Ala Leu Lys 400 405 410 415	1307
gac tgt gag gaa tgt atc cag ctg gag ccg acc ttc atc aag ggt tat Asp Cys Glu Glu Cys Ile Gln Leu Glu Pro Thr Phe Ile Lys Gly Tyr 420 425 430	1355
aca cgg aaa gcc gct gcg ctg gaa gcg atg aag gac tac acc aaa gcc Thr Arg Lys Ala Ala Ala Leu Glu Ala Met Lys Asp Tyr Thr Lys Ala 435 440 445	1403
atg gat gtg tac cag aag gcg cta gac ctg gac tcc agc tgt aag gag Met Asp Val Tyr Gln Lys Ala Leu Asp Leu Asp Ser Ser Cys Lys Glu 450 455 460	1451
gcg gca gac ggc tac cag cgc tgt atg atg gcg cag tac aac cgg cac Ala Ala Asp Gly Tyr Gln Arg Cys Met Met Ala Gln Tyr Asn Arg His 465 470 475	1499
gac agc ccc gaa gat gtg aag cga cga gcc atg gcc gac cct gag gtg Asp Ser Pro Glu Asp Val Lys Arg Arg Ala Met Ala Asp Pro Glu Val 480 485 490 495	1547
cag cag atc atg agt gac cca gcc atg cgc ctt atc ctg gaa cag atg Gln Gln Ile Met Ser Asp Pro Ala Met Arg Leu Ile Leu Glu Gln Met 500 505 510	1595
cag aag gac ccc cag gca ctc agc gaa cac tta aag aat cct gta ata Gln Lys Asp Pro Gln Ala Leu Ser Glu His Leu Lys Asn Pro Val Ile 42/201	1643

515	520	525	
gca cag aag atc cag aag ctg atg gat gtg ggt ctg att gca att cgg			1691
Ala Gln Lys Ile Gln Lys Leu Met Asp Val Gly Leu Ile Ala Ile Arg			
530	535	540	
tga tgacttggtc atccccctt cccttcgccc tcatgtggaa agaggagctg			1744
ggaccgcggc gagcagcacg gagcggaagg gagagcaggg gagagaaggc ctcattcttc			1804
tatatattata cataaccccg gggaagacac agagactcgt acctgcgctg tttgtgccgc			1864
cgctgcctct gggccctccc agcacacgca tggctctctc accgctgccc tcgagttcca			1924
tgtctctttc ccctgcccct agttgctgtc tcggctgctc tcccatagtt gggttttttt			1984
ttatttgggg cagtgggcat gttatgggga ggggaggggg ttcttccagc ctcaggctcc			2044
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ggttataac			2113

<210> 16
 <211> 543
 <212> PRT
 <213> Homo sapiens

<400> 16

Met	Glu	Gln	Val	Asn	Glu	Leu	Lys	Glu	Lys	Gly	Asn	Lys	Ala	Leu	Ser
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Val	Gly	Asn	Ile	Asp	Asp	Ala	Leu	Gln	Cys	Tyr	Ser	Glu	Ala	Ile	Lys
		20						25					30		

Leu	Asp	Pro	His	Asn	His	Val	Leu	Tyr	Ser	Asn	Arg	Ser	Ala	Ala	Tyr
	35						40					45			

Ala	Lys	Lys	Gly	Asp	Tyr	Gln	Lys	Ala	Tyr	Glu	Asp	Gly	Cys	Lys	Thr
50						55				60					

Val	Asp	Leu	Lys	Pro	Asp	Trp	Gly	Lys	Gly	Tyr	Ser	Arg	Lys	Ala	Ala
65					70				75					80	

Ala Leu Glu Phe Leu Asn Arg Phe Glu Glu Ala Lys Arg Thr Tyr Glu
85 90 95

Glu Gly Leu Lys His Glu Ala Asn Asn Pro Gln Leu Lys Glu Gly Leu
100 105 110

Gln Asn Met Glu Ala Arg Leu Ala Glu Arg Lys Phe Met Asn Pro Phe
115 120 125

Asn Met Pro Asn Leu Tyr Gln Lys Leu Glu Ser Asp Pro Arg Thr Arg
130 135 140

Thr Leu Leu Ser Asp Pro Thr Tyr Arg Glu Leu Ile Glu Gln Leu Arg
145 150 155 160

Asn Lys Pro Ser Asp Leu Gly Thr Lys Leu Gln Asp Pro Arg Ile Met
165 170 175

Thr Thr Leu Ser Val Leu Leu Gly Val Asp Leu Gly Ser Met Asp Glu
180 185 190

Glu Glu Glu Ile Ala Thr Pro Pro Pro Pro Pro Pro Lys Lys Glu
195 200 205

Thr Lys Pro Glu Pro Met Glu Glu Asp Leu Pro Glu Asn Lys Lys Gln
210 215 220

Ala Leu Lys Glu Lys Glu Leu Gly Asn Asp Ala Tyr Lys Lys Lys Asp
225 230 235 240

Phe Asp Thr Ala Leu Lys His Tyr Asp Lys Ala Lys Glu Leu Asp Pro
245 250 255

Thr Asn Met Thr Tyr Ile Thr Asn Gln Ala Ala Val Tyr Phe Glu Lys
260 265 270

Gly Asp Tyr Asn Lys Cys Arg Glu Leu Cys Glu Lys Ala Ile Glu Val
275 280 285

Gly Arg Glu Asn Arg Glu Asp Tyr Arg Gln Ile Ala Lys Ala Tyr Ala
290 295 300

Arg Ile Gly Asn Ser Tyr Phe Lys Glu Glu Lys Tyr Lys Asp Ala Ile
305 310 315 320

His Phe Tyr Asn Lys Ser Leu Ala Glu His Arg Thr Pro Asp Val Leu
325 330 335

Lys Lys Cys Gln Gln Ala Glu Lys Ile Leu Lys Glu Gln Glu Arg Leu
340 345 350

Ala Tyr Ile Asn Pro Asp Leu Ala Leu Glu Glu Lys Asn Lys Gly Asn
355 360 365

Glu Cys Phe Gln Lys Gly Asp Tyr Pro Gln Ala Met Lys His Tyr Thr
370 375 380

Glu Ala Ile Lys Arg Asn Pro Lys Asp Ala Lys Leu Tyr Ser Asn Arg
385 390 395 400

Ala Ala Cys Tyr Thr Lys Leu Leu Glu Phe Gln Leu Ala Leu Lys Asp
405 410 415

Cys Glu Glu Cys Ile Gln Leu Glu Pro Thr Phe Ile Lys Gly Tyr Thr
420 425 430

Arg Lys Ala Ala Ala Leu Glu Ala Met Lys Asp Tyr Thr Lys Ala Met
435 440 445

Asp Val Tyr Gln Lys Ala Leu Asp Leu Asp Ser Ser Cys Lys Glu Ala
450 455 460

Ala Asp Gly Tyr Gln Arg Cys Met Met Ala Gln Tyr Asn Arg His Asp
465 470 475 480

Ser Pro Glu Asp Val Lys Arg Arg Ala Met Ala Asp Pro Glu Val Gln
485 490 495

Gln Ile Met Ser Asp Pro Ala Met Arg Leu Ile Leu Glu Gln Met Gln
500 505 510

Lys Asp Pro Gln Ala Leu Ser Glu His Leu Lys Asn Pro Val Ile Ala
515 520 525

Gln Lys Ile Gln Lys Leu Met Asp Val Gly Leu Ile Ala Ile Arg
530 535 540

<210> 17
<211> 2033
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (29)..(1705)
<223>

<400> 17
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ggc gga ggc ggc ggt ggc cgc tac tac ggc ggc ggc agt gag ggc ggc 100
Gly Gly Gly Gly Gly Gly Arg Tyr Tyr Gly Gly Gly Ser Glu Gly Gly
10 15 20

cgg gcc cct aag cgg ctc aag act gac aac gcc ggc gac cag cac gga 148
Arg Ala Pro Lys Arg Leu Lys Thr Asp Asn Ala Gly Asp Gln His Gly
25 30 35 40

ggc ggc ggc ggt ggc ggt gga gga gcc ggg gcg gcg ggc ggc ggc ggc 196
Gly Gly Gly Gly Gly Gly Gly Gly Ala Gly Ala Ala Gly Gly Gly Gly
45 50 55

ggt ggg gag aac tac gat gac ccg cac aaa acc cct gcc tcc cca gtt 244
Gly Gly Glu Asn Tyr Asp Asp Pro His Lys Thr Pro Ala Ser Pro Val
60 65 70

gtc cac atc agg ggc ctg att gac ggt gtg gtg gaa gca gac ctt gtg 292
Val His Ile Arg Gly Leu Ile Asp Gly Val Val Glu Ala Asp Leu Val
75 80 85

gag gcc ttg cag gag ttt gga ccc atc agc tat gtg gtg gta atg cct Glu Ala Leu Gln Glu Phe Gly Pro Ile Ser Tyr Val Val Val Met Pro 90 95 100	340
aaa aag aga caa gca ctg gtg gag ttt gaa gat gtg ttg ggg gct tgc Lys Lys Arg Gln Ala Leu Val Glu Phe Glu Asp Val Leu Gly Ala Cys 105 110 115 120	388
aac gca gtg aac tac gca gcc gac aac caa ata tac att gct ggt cac Asn Ala Val Asn Tyr Ala Ala Asp Asn Gln Ile Tyr Ile Ala Gly His 125 130 135	436
cca gct ttt gtc aac tac tct acc agc cag aag atc tcc cgc cct ggg Pro Ala Phe Val Asn Tyr Ser Thr Ser Gln Lys Ile Ser Arg Pro Gly 140 145 150	484
gac tcg gat gac tcc cgg agc gtg aac agt gtg ctt ctc ttt acc atc Asp Ser Asp Asp Ser Arg Ser Val Asn Ser Val Leu Leu Phe Thr Ile 155 160 165	532
ctg aac ccc att tat tcg atc acc acg gat gtt ctt tac act atc tgt Leu Asn Pro Ile Tyr Ser Ile Thr Thr Asp Val Leu Tyr Thr Ile Cys 170 175 180	580
aat cct tgt ggc cct gtc cag aga att gtc att ttc agg aag aat gga Asn Pro Cys Gly Pro Val Gln Arg Ile Val Ile Phe Arg Lys Asn Gly 185 190 195 200	628
gtt cag gcg atg gtg gaa ttt gac tca gtt caa agt gcc cag cgg gcc Val Gln Ala Met Val Glu Phe Asp Ser Val Gln Ser Ala Gln Arg Ala 205 210 215	676
aag gcc tct ctc aat ggg gct gat atc tat tct ggc tgt tgc act ctg Lys Ala Ser Leu Asn Gly Ala Asp Ile Tyr Ser Gly Cys Cys Thr Leu 220 225 230	724
aag atc gaa tac gca aag cct aca cgc ttg aat gtg ttc aag aat gat Lys Ile Glu Tyr Ala Lys Pro Thr Arg Leu Asn Val Phe Lys Asn Asp 235 240 245	772
cag gat act tgg gac tac aca aac ccc aat ctc agt gga caa ggt gac Gln Asp Thr Trp Asp Tyr Thr Asn Pro Asn Leu Ser Gly Gln Gly Asp 250 255 260	820
cct ggc agc aac ccc aac aaa cgc cag agg cag ccc cct ctc ctg gga Pro Gly Ser Asn Pro Asn Lys Arg Gln Arg Gln Pro Pro Leu Leu Gly 265 270 275 280	868
gat cac ccc gca gaa tat gga ggg ccc cac ggt ggg tac cac agc cat 47/201	916

Asp	His	Pro	Ala	Glu	Tyr	Gly	Gly	Pro	His	Gly	Gly	Tyr	His	Ser	His		
				285					290					295			
tac	cat	gat	gag	ggc	tac	ggg	ccc	ccc	cca	cct	cac	tac	gaa	ggg	aga		964
Tyr	His	Asp	Glu	Gly	Tyr	Gly	Pro	Pro	Pro	Pro	His	Tyr	Glu	Gly	Arg		
			300				305						310				
agg	atg	ggt	cca	cca	gtg	ggg	ggt	cac	cgt	cgg	ggc	cca	agt	cgc	tac		1012
Arg	Met	Gly	Pro	Pro	Val	Gly	Gly	His	Arg	Arg	Gly	Pro	Ser	Arg	Tyr		
		315					320					325					
ggc	ccc	cag	tat	ggg	cac	ccc	cca	ccc	cct	ccc	cca	cca	ccc	gag	tat		1060
Gly	Pro	Gln	Tyr	Gly	His	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Tyr		
	330					335					340						
ggc	cct	cac	gcc	gac	agc	cct	gtg	ctc	atg	gtc	tat	ggc	ttg	gat	caa		1108
Gly	Pro	His	Ala	Asp	Ser	Pro	Val	Leu	Met	Val	Tyr	Gly	Leu	Asp	Gln		
345					350					355					360		
tct	aag	atg	aac	ggt	gac	cga	gtc	ttc	aat	gtc	ttc	tgc	tta	tat	ggc		1156
Ser	Lys	Met	Asn	Gly	Asp	Arg	Val	Phe	Asn	Val	Phe	Cys	Leu	Tyr	Gly		
				365					370					375			
aat	gtg	gag	aag	gtg	aaa	ttc	atg	aaa	agc	aag	ccg	ggg	gcc	gcc	atg		1204
Asn	Val	Glu	Lys	Val	Lys	Phe	Met	Lys	Ser	Lys	Pro	Gly	Ala	Ala	Met		
			380					385					390				
gtg	gag	atg	gct	gat	ggc	tac	gct	gta	gac	cgg	gcc	att	acc	cac	ctc		1252
Val	Glu	Met	Ala	Asp	Gly	Tyr	Ala	Val	Asp	Arg	Ala	Ile	Thr	His	Leu		
		395					400					405					
aac	aac	aac	ttc	atg	ttt	ggg	cag	aag	ctg	aat	gtc	tgt	gtc	tcc	aag		1300
Asn	Asn	Asn	Phe	Met	Phe	Gly	Gln	Lys	Leu	Asn	Val	Cys	Val	Ser	Lys		
	410					415					420						
cag	cca	gcc	atc	atg	cct	ggt	cag	tca	tac	ggg	ttg	gaa	gac	ggg	tct		1348
Gln	Pro	Ala	Ile	Met	Pro	Gly	Gln	Ser	Tyr	Gly	Leu	Glu	Asp	Gly	Ser		
425					430					435					440		
tgc	agt	tac	aaa	gac	ttc	agt	gaa	tcc	cgg	aac	aat	cgg	ttc	tcc	acc		1396
Cys	Ser	Tyr	Lys	Asp	Phe	Ser	Glu	Ser	Arg	Asn	Asn	Arg	Phe	Ser	Thr		
				445					450					455			
cca	gag	cag	gca	gcc	aag	aac	cgc	atc	cag	cac	ccc	agc	aac	gtg	ctg		1444
Pro	Glu	Gln	Ala	Ala	Lys	Asn	Arg	Ile	Gln	His	Pro	Ser	Asn	Val	Leu		
			460					465					470				
cac	ttc	ttc	aac	gcc	ccg	ctg	gag	gtg	acc	gag	gag	aac	ttc	ttt	gag		1492
His	Phe	Phe	Asn	Ala	Pro	Leu	Glu	Val	Thr	Glu	Glu	Asn	Phe	Phe	Glu		
		475					480					485					

atc tgc gat gag ctg gga gtg aag cgg cca tct tct gtg aaa gta ttc 1540
 Ile Cys Asp Glu Leu Gly Val Lys Arg Pro Ser Ser Val Lys Val Phe
 490 495 500

tca ggc aaa agt gag cgc agc tcc tct gga ctg ctg gag tgg gaa tcc 1588
 Ser Gly Lys Ser Glu Arg Ser Ser Ser Gly Leu Leu Glu Trp Glu Ser
 505 510 515 520

aag agc gat gcc ctg gag act ctg ggc ttc ctg aac cat tac cag atg 1636
 Lys Ser Asp Ala Leu Glu Thr Leu Gly Phe Leu Asn His Tyr Gln Met
 525 530 535

aaa aac cca aat ggt cca tac cct tac act ctg aag ttg tgt ttc tcc 1684
 Lys Asn Pro Asn Gly Pro Tyr Pro Tyr Thr Leu Lys Leu Cys Phe Ser
 540 545 550

act gct cag cac gcc tcc taa ttaggtgcct aggaagagtc ccatctgagc 1735
 Thr Ala Gln His Ala Ser
 555

aggaagacat ttctctttcc tttatgccat tttttgtttt tgttatttgc aaaagatcct 1795

gtattccttt tttttttttt ttttttttaa atgctagggt tgtagaggct tacttaacct 1855

taatggaaac gctggaaatc tgcaggggga gggagagggg aactgttata tcccaagatt 1915

aaccttcact tttaaaaaat tattgtacat gtgatTTTTT tttttcctgt tcatacattt 1975

gtgctgcccc tgtagctcttg gcacatttca ataaaattgt ttggaaaata aacacagc 2033

<210> 18
 <211> 558
 <212> PRT
 <213> Homo sapiens

<400> 18

Met Val Lys Met Ala Ala Ala Gly Gly Gly Gly Gly Gly Gly Arg Tyr
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Tyr Gly Gly Gly Ser Glu Gly Gly Arg Ala Pro Lys Arg Leu Lys Thr
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Asp Asn Ala Gly Asp Gln His Gly Gly Gly Gly Gly Gly Gly Gly Gly
 35 40 45

Ala Gly Ala Ala Gly Gly Gly Gly Gly Glu Asn Tyr Asp Asp Pro
50 55 60

His Lys Thr Pro Ala Ser Pro Val Val His Ile Arg Gly Leu Ile Asp
65 70 75 80

Gly Val Val Glu Ala Asp Leu Val Glu Ala Leu Gln Glu Phe Gly Pro
85 90 95

Ile Ser Tyr Val Val Val Met Pro Lys Lys Arg Gln Ala Leu Val Glu
100 105 110

Phe Glu Asp Val Leu Gly Ala Cys Asn Ala Val Asn Tyr Ala Ala Asp
115 120 125

Asn Gln Ile Tyr Ile Ala Gly His Pro Ala Phe Val Asn Tyr Ser Thr
130 135 140

Ser Gln Lys Ile Ser Arg Pro Gly Asp Ser Asp Asp Ser Arg Ser Val
145 150 155 160

Asn Ser Val Leu Leu Phe Thr Ile Leu Asn Pro Ile Tyr Ser Ile Thr
165 170 175

Thr Asp Val Leu Tyr Thr Ile Cys Asn Pro Cys Gly Pro Val Gln Arg
180 185 190

Ile Val Ile Phe Arg Lys Asn Gly Val Gln Ala Met Val Glu Phe Asp
195 200 205

Ser Val Gln Ser Ala Gln Arg Ala Lys Ala Ser Leu Asn Gly Ala Asp
210 215 220

Ile Tyr Ser Gly Cys Cys Thr Leu Lys Ile Glu Tyr Ala Lys Pro Thr
225 230 235 240

Arg Leu Asn Val Phe Lys Asn Asp Gln Asp Thr Trp Asp Tyr Thr Asn
50/201

	245		250		255
Pro Asn Leu Ser Gly Gln Gly Asp Pro Gly Ser Asn Pro Asn Lys Arg	260		265		270
Gln Arg Gln Pro Pro Leu Leu Gly Asp His Pro Ala Glu Tyr Gly Gly	275		280		285
Pro His Gly Gly Tyr His Ser His Tyr His Asp Glu Gly Tyr Gly Pro	290		295		300
Pro Pro Pro His Tyr Glu Gly Arg Arg Met Gly Pro Pro Val Gly Gly	305		310		315
His Arg Arg Gly Pro Ser Arg Tyr Gly Pro Gln Tyr Gly His Pro Pro	325		330		335
Pro Pro Pro Pro Pro Pro Glu Tyr Gly Pro His Ala Asp Ser Pro Val	340		345		350
Leu Met Val Tyr Gly Leu Asp Gln Ser Lys Met Asn Gly Asp Arg Val	355		360		365
Phe Asn Val Phe Cys Leu Tyr Gly Asn Val Glu Lys Val Lys Phe Met	370		375		380
Lys Ser Lys Pro Gly Ala Ala Met Val Glu Met Ala Asp Gly Tyr Ala	385		390		395
Val Asp Arg Ala Ile Thr His Leu Asn Asn Asn Phe Met Phe Gly Gln	405		410		415
Lys Leu Asn Val Cys Val Ser Lys Gln Pro Ala Ile Met Pro Gly Gln	420		425		430
Ser Tyr Gly Leu Glu Asp Gly Ser Cys Ser Tyr Lys Asp Phe Ser Glu	435		440		445

Ser Arg Asn Asn Arg Phe Ser Thr Pro Glu Gln Ala Ala Lys Asn Arg
 450 455 460

Ile Gln His Pro Ser Asn Val Leu His Phe Phe Asn Ala Pro Leu Glu
 465 470 475 480

Val Thr Glu Glu Asn Phe Phe Glu Ile Cys Asp Glu Leu Gly Val Lys
 485 490 495

Arg Pro Ser Ser Val Lys Val Phe Ser Gly Lys Ser Glu Arg Ser Ser
 500 505 510

Ser Gly Leu Leu Glu Trp Glu Ser Lys Ser Asp Ala Leu Glu Thr Leu
 515 520 525

Gly Phe Leu Asn His Tyr Gln Met Lys Asn Pro Asn Gly Pro Tyr Pro
 530 535 540

Tyr Thr Leu Lys Leu Cys Phe Ser Thr Ala Gln His Ala Ser
 545 550 555

<210> 19
 <211> 3465
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (219).. (2639)
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<400> 19
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 cgcccggggc gaggagcagc cgcagcagcc gccaccagtg gccgagttag cggagccgag 180
 tttaggcag cgcctagcgg tgaatcgggg ccctcacc atg agt tcc tcg cct gtt 236
 Met Ser Ser Ser Pro Val
 1 5

aat gta aaa aag ctg aag gtg tcg gag ctg aaa gag gag ctc aag aag	284
Asn Val Lys Lys Leu Lys Val Ser Glu Leu Lys Glu Glu Leu Lys Lys	
10 15 20	
cga cgc ctt tct gac aag ggt ctc aag gcc gag ctc atg gag cga ctc	332
Arg Arg Leu Ser Asp Lys Gly Leu Lys Ala Glu Leu Met Glu Arg Leu	
25 30 35	
cag gct gcg ctg gac gac gag gag gcc ggg ggc cgc ccc gcc atg gag	380
Gln Ala Ala Leu Asp Asp Glu Glu Ala Gly Gly Arg Pro Ala Met Glu	
40 45 50	
ccc ggg aac ggc agc cta gac ctg ggc ggg gat tcc gct ggg cgc tcg	428
Pro Gly Asn Gly Ser Leu Asp Leu Gly Gly Asp Ser Ala Gly Arg Ser	
55 60 65 70	
gga gca ggc ctc gag cag gag gcc gcg gcc ggc ggc gat gaa gag gag	476
Gly Ala Gly Leu Glu Gln Glu Ala Ala Ala Gly Gly Asp Glu Glu Glu	
75 80 85	
gag gaa gag gaa gag gag gag gaa gga atc tcc gct ctg gac ggc gac	524
Glu Glu Glu Glu Glu Glu Glu Glu Gly Ile Ser Ala Leu Asp Gly Asp	
90 95 100	
cag atg gag cta gga gag gag aac ggg gcc gcg ggg gcg gcc gac tcg	572
Gln Met Glu Leu Gly Glu Glu Asn Gly Ala Ala Gly Ala Ala Asp Ser	
105 110 115	
ggc ccg atg gag gag gag gag gcc gcc tcg gaa gac gag aac ggc gac	620
Gly Pro Met Glu Glu Glu Glu Ala Ala Ser Glu Asp Glu Asn Gly Asp	
120 125 130	
gat cag ggt ttc cag gaa ggg gaa gat gag ctc ggg gac gaa gag gaa	668
Asp Gln Gly Phe Gln Glu Gly Glu Asp Glu Leu Gly Asp Glu Glu Glu	
135 140 145 150	
ggc gcg ggc gac gag aac ggg cac ggg gag cag cag cct caa ccg ccg	716
Gly Ala Gly Asp Glu Asn Gly His Gly Glu Gln Gln Pro Gln Pro Pro	
155 160 165	
gcg acg cag cag caa cag ccc caa cag cag cgc ggg gcc gcc aag gag	764
Ala Thr Gln Gln Gln Gln Pro Gln Gln Gln Arg Gly Ala Ala Lys Glu	
170 175 180	
gcc gcg ggg aag agc agc ggc ccc acc tcg ctg ttc gcg gtg acg gtg	812
Ala Ala Gly Lys Ser Ser Gly Pro Thr Ser Leu Phe Ala Val Thr Val	
185 190 195	
gcg ccg ccc ggg gcg agg cag ggc cag cag cag gcg gga ggg gac ggc	860
Ala Pro Pro Gly Ala Arg Gln Gly Gln Gln Gln Ala Gly Gly Asp Gly	

200	205	210	
aaa aca gaa cag Lys Thr Glu Gln 215	aaa ggc gga gat Lys Gly Gly Asp 220	aaa aag agg ggt gtt Lys Lys Arg Gly Val 225	aga cca Arg Pro 230
908			
cga gaa gat cat Arg Glu Asp 235	ggc cgt gga tat Gly Arg Gly Tyr 240	ttt gag tac att Phe Glu Tyr Ile 245	aag Asn Lys 245
956			
tat agc aga gcc Tyr Ser Arg Ala 250	aaa tct cct cag Lys Ser Pro Gln 255	cct gtt gaa gaa gaa Pro Pro Val Glu Glu Glu 260	gat gaa Asp Glu 260
1004			
cac ttc gat gac His Phe Asp Asp 265	aca gtg gtt tgt Thr Val Val Cys 270	ctt gat act tat Leu Asp Thr Tyr 275	cta Leu 275
1052			
cat ttt aaa ata His Phe Lys Ile 280	tca aga gat cgt Ser Arg Asp Arg 285	ctc agt gct tct Leu Ser Ala Ser 290	tcc ctt aca atg Ser Leu Thr Met 290
1100			
gag agt ttt gct Glu Ser Phe Ala 295	ttt ctt tgg gct Phe Leu Trp Ala 300	gga gga aga gca Gly Gly Arg Ala 305	tcc tat ggt gtg Ser Tyr Gly Val 310
1148			
tca aaa ggc aaa Ser Lys Gly Lys 315	gtg tgt ttt gag Val Cys Phe Glu 320	atg aag gtt aca Met Lys Val Thr 325	gag aag atc cca Glu Lys Ile Pro 325
1196			
gta agg cat tta Val Arg His Leu 330	tat aca aaa gat Tyr Thr Lys Asp 335	att gac ata cat Ile Asp Ile His 340	gaa gtt cgt att Glu Val Arg Ile 340
1244			
ggc tgg tca cta Gly Trp Ser Leu 345	act aca agt gga Thr Thr Ser Gly 350	atg tta ctt ggt Met Leu Leu Gly 355	gaa gaa gaa ttt Glu Glu Glu Phe 355
1292			
tct tat ggg tat Ser Tyr Gly Tyr 360	tct cta aaa gga Ser Leu Lys Gly 365	ata aaa aca tgc Ile Lys Thr Cys 370	aac tgt gag act Asn Cys Glu Thr 370
1340			
gaa gat tat gga Glu Asp Tyr Gly 375	gaa aag ttt gat Glu Lys Phe Asp 380	gaa aat gat gtg Glu Asn Asp Val 385	att aca tgt ttt Ile Thr Cys Phe 390
1388			
gct aac ttt gaa Ala Asn Phe Glu 395	agt gat gaa gta Ser Asp Glu Val 400	ctc tcg tat gct Leu Ser Tyr Ala 405	aag aat gga Lys Asn Gly 405
1436			

caa gat ctt ggc gtt gcc ttc aaa atc agt aag gaa gtt ctt gct gga Gln Asp Leu Gly Val Ala Phe Lys Ile Ser Lys Glu Val Leu Ala Gly 410 415 420	1484
cgg cca ctg ttc ccg cat gtt ctc tgc cac aac tgt gca gtt gaa ttt Arg Pro Leu Phe Pro His Val Leu Cys His Asn Cys Ala Val Glu Phe 425 430 435	1532
aat ttt ggt cag aag gaa aag cca tat ttt cca ata cct gaa gag tat Asn Phe Gly Gln Lys Glu Lys Pro Tyr Phe Pro Ile Pro Glu Glu Tyr 440 445 450	1580
act ttc atc cag aac gtc ccc tta gag gat cga gtt aga gga cca aag Thr Phe Ile Gln Asn Val Pro Leu Glu Asp Arg Val Arg Gly Pro Lys 455 460 465 470	1628
ggg cct gaa gag aag aaa gat tgt gaa gtt gtg atg atg att ggc ttg Gly Pro Glu Glu Lys Lys Asp Cys Glu Val Val Met Met Ile Gly Leu 475 480 485	1676
cca gga gct gga aaa act acc tgg gtt act aaa cat gca gca gaa aat Pro Gly Ala Gly Lys Thr Thr Trp Val Thr Lys His Ala Ala Glu Asn 490 495 500	1724
cca ggg aaa tat aac att ctt ggc aca aat act att atg gat aag atg Pro Gly Lys Tyr Asn Ile Leu Gly Thr Asn Thr Ile Met Asp Lys Met 505 510 515	1772
atg gtg gca ggt ttt aag aag caa atg gca gat act gga aaa ctg aac Met Val Ala Gly Phe Lys Lys Gln Met Ala Asp Thr Gly Lys Leu Asn 520 525 530	1820
aca ctg ttg cag aga gcc ccc cag tgt ctt ggg aaa ttt att gag att Thr Leu Leu Gln Arg Ala Pro Gln Cys Leu Gly Lys Phe Ile Glu Ile 535 540 545 550	1868
gct gcc cga aag aag cga aat ttt att ctg gat cag aca aat gtg tct Ala Ala Arg Lys Lys Arg Asn Phe Ile Leu Asp Gln Thr Asn Val Ser 555 560 565	1916
gct gct gcc cag agg aga aaa atg tgc ctg ttt gca ggc ttc cag cga Ala Ala Ala Gln Arg Arg Lys Met Cys Leu Phe Ala Gly Phe Gln Arg 570 575 580	1964
aaa gct gtt gta gtt tgc cca aaa gat gaa gac tat aag caa aga aca Lys Ala Val Val Val Cys Pro Lys Asp Glu Asp Tyr Lys Gln Arg Thr 585 590 595	2012
cag aag aaa gca gaa gta gag ggg aaa gac cta cca gaa cat gcg gtc Gln Lys Lys Ala Glu Val Glu Gly Lys Asp Leu Pro Glu His Ala Val 55/201	2060

600	605	610	
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Leu Lys Met Lys Gly Asn Phe Thr Leu Pro Glu Val Ala Glu Cys Phe			
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gat gaa ata acc tat gtt gaa ctt cag aag gaa gaa gcc caa aaa ctc			2156
Asp Glu Ile Thr Tyr Val Glu Leu Gln Lys Glu Glu Ala Gln Lys Leu			
	635	640	645
ttg gag caa tat aag gaa gaa agc aaa aag gct ctt cca cca gaa aag			2204
Leu Glu Gln Tyr Lys Glu Glu Ser Lys Lys Ala Leu Pro Pro Glu Lys			
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aaa cag aac act ggc tca aag aaa agc aat aaa aat aag agt ggc aag			2252
Lys Gln Asn Thr Gly Ser Lys Lys Ser Asn Lys Asn Lys Ser Gly Lys			
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aac cag ttt aac aga ggt ggt ggc cat aga gga cgt gga gga ttc aat			2300
Asn Gln Phe Asn Arg Gly Gly Gly His Arg Gly Arg Gly Gly Phe Asn			
	680	685	690
atg cgt ggt gga aat ttc aga gga gga gcc cct ggg aat cgt ggc gga			2348
Met Arg Gly Gly Asn Phe Arg Gly Gly Ala Pro Gly Asn Arg Gly Gly			
695	700	705	710
tat aat agg agg ggc aac atg cca cag aga ggt ggt ggc ggt gga gga			2396
Tyr Asn Arg Arg Gly Asn Met Pro Gln Arg Gly Gly Gly Gly Gly Gly			
	715	720	725
agt ggt gga atc ggc tat cca tac cct cgt gcc cct gtt ttt cct ggc			2444
Ser Gly Gly Ile Gly Tyr Pro Tyr Pro Arg Ala Pro Val Phe Pro Gly			
	730	735	740
cgt ggt agt tac tca aac aga ggg aac tac aac aga ggt gga atg ccc			2492
Arg Gly Ser Tyr Ser Asn Arg Gly Asn Tyr Asn Arg Gly Gly Met Pro			
	745	750	755
aac aga ggg aac tac aac cag aac ttc aga gga cga gga aac aat cgt			2540
Asn Arg Gly Asn Tyr Asn Gln Asn Phe Arg Gly Arg Gly Asn Asn Arg			
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ggc tac aaa aat caa tct cag ggc tac aac cag tgg cag cag ggt caa			2588
Gly Tyr Lys Asn Gln Ser Gln Gly Tyr Asn Gln Trp Gln Gln Gly Gln			
775	780	785	790
ttc tgg ggt cag aag cca tgg agt cag cat tat cac caa gga tat tat			2636
Phe Trp Gly Gln Lys Pro Trp Ser Gln His Tyr His Gln Gly Tyr Tyr			
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Glu	Leu	Met	Glu	Arg	Leu	Gln	Ala	Ala	Leu	Asp	Asp	Glu	Glu	Ala	Gly
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Gly	Arg	Pro	Ala	Met	Glu	Pro	Gly	Asn	Gly	Ser	Leu	Asp	Leu	Gly	Gly
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Asp Ser Ala Gly Arg Ser Gly Ala Gly Leu Glu Gln Glu Ala Ala Ala
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Gly Gly Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Ile
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Ser Ala Leu Asp Gly Asp Gln Met Glu Leu Gly Glu Glu Asn Gly Ala
100 105 110

Ala Gly Ala Ala Asp Ser Gly Pro Met Glu Glu Glu Glu Ala Ala Ser
115 120 125

Glu Asp Glu Asn Gly Asp Asp Gln Gly Phe Gln Glu Gly Glu Asp Glu
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Leu Gly Asp Glu Glu Glu Gly Ala Gly Asp Glu Asn Gly His Gly Glu
145 150 155 160

Gln Gln Pro Gln Pro Pro Ala Thr Gln Gln Gln Gln Pro Gln Gln Gln
165 170 175

Arg Gly Ala Ala Lys Glu Ala Ala Gly Lys Ser Ser Gly Pro Thr Ser
180 185 190

Leu Phe Ala Val Thr Val Ala Pro Pro Gly Ala Arg Gln Gly Gln Gln
195 200 205

Gln Ala Gly Gly Asp Gly Lys Thr Glu Gln Lys Gly Gly Asp Lys Lys
210 215 220

Arg Gly Val Lys Arg Pro Arg Glu Asp His Gly Arg Gly Tyr Phe Glu
225 230 235 240

Tyr Ile Glu Glu Asn Lys Tyr Ser Arg Ala Lys Ser Pro Gln Pro Pro
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Val Glu Glu Glu Asp Glu His Phe Asp Asp Thr Val Val Cys Leu Asp
260 265 270

Thr Tyr Asn Cys Asp Leu His Phe Lys Ile Ser Arg Asp Arg Leu Ser
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Arg Ala Ser Tyr Gly Val Ser Lys Gly Lys Val Cys Phe Glu Met Lys
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Val Thr Glu Lys Ile Pro Val Arg His Leu Tyr Thr Lys Asp Ile Asp
325 330 335

Ile His Glu Val Arg Ile Gly Trp Ser Leu Thr Thr Ser Gly Met Leu
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Leu Gly Glu Glu Glu Phe Ser Tyr Gly Tyr Ser Leu Lys Gly Ile Lys
355 360 365

Thr Cys Asn Cys Glu Thr Glu Asp Tyr Gly Glu Lys Phe Asp Glu Asn
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Asp Val Ile Thr Cys Phe Ala Asn Phe Glu Ser Asp Glu Val Glu Leu
385 390 395 400

Ser Tyr Ala Lys Asn Gly Gln Asp Leu Gly Val Ala Phe Lys Ile Ser
405 410 415

Lys Glu Val Leu Ala Gly Arg Pro Leu Phe Pro His Val Leu Cys His
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Asn Cys Ala Val Glu Phe Asn Phe Gly Gln Lys Glu Lys Pro Tyr Phe
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Pro Ile Pro Glu Glu Tyr Thr Phe Ile Gln Asn Val Pro Leu Glu Asp
450 455 460

Arg Val Arg Gly Pro Lys Gly Pro Glu Glu Lys Lys Asp Cys Glu Val
465 470 475 480

Val Met Met Ile Gly Leu Pro Gly Ala Gly Lys Thr Thr Trp Val Thr
485 490 495

Lys His Ala Ala Glu Asn Pro Gly Lys Tyr Asn Ile Leu Gly Thr Asn
500 505 510

Thr Ile Met Asp Lys Met Met Val Ala Gly Phe Lys Lys Gln Met Ala
515 520 525

Asp Thr Gly Lys Leu Asn Thr Leu Leu Gln Arg Ala Pro Gln Cys Leu
530 535 540

Gly Lys Phe Ile Glu Ile Ala Ala Arg Lys Lys Arg Asn Phe Ile Leu
545 550 555 560

Asp Gln Thr Asn Val Ser Ala Ala Ala Gln Arg Arg Lys Met Cys Leu
565 570 575

Phe Ala Gly Phe Gln Arg Lys Ala Val Val Val Cys Pro Lys Asp Glu
580 585 590

Asp Tyr Lys Gln Arg Thr Gln Lys Lys Ala Glu Val Glu Gly Lys Asp
595 600 605

Leu Pro Glu His Ala Val Leu Lys Met Lys Gly Asn Phe Thr Leu Pro
610 615 620

Glu Val Ala Glu Cys Phe Asp Glu Ile Thr Tyr Val Glu Leu Gln Lys
625 630 635 640

Glu Glu Ala Gln Lys Leu Leu Glu Gln Tyr Lys Glu Glu Ser Lys Lys
645 650 655

Ala Leu Pro Pro Glu Lys Lys Gln Asn Thr Gly Ser Lys Lys Ser Asn
660 665 670

Lys Asn Lys Ser Gly Lys Asn Gln Phe Asn Arg Gly Gly Gly His Arg
675 680 685

Gly Arg Gly Gly Phe Asn Met Arg Gly Gly Asn Phe Arg Gly Gly Ala
690 695 700

Pro Gly Asn Arg Gly Gly Tyr Asn Arg Arg Gly Asn Met Pro Gln Arg
705 710 715 720

Gly Gly Gly Gly Gly Gly Ser Gly Gly Ile Gly Tyr Pro Tyr Pro Arg
725 730 735

Ala Pro Val Phe Pro Gly Arg Gly Ser Tyr Ser Asn Arg Gly Asn Tyr
740 745 750

Asn Arg Gly Gly Met Pro Asn Arg Gly Asn Tyr Asn Gln Asn Phe Arg
755 760 765

Gly Arg Gly Asn Asn Arg Gly Tyr Lys Asn Gln Ser Gln Gly Tyr Asn
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ccttattgat cctttttctt ggcgttacca tttttgaagc aaagttaacc tagctttcta 240

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Arg Asp Ser Gln Gly His Gly Arg Asp Leu Ser Ala Ala Gly Ile Gly
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Leu Leu Ala Ala Ala Thr Gln Ser Leu Ser Met Pro Ala Ser Leu Gly
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agg atg aac cag ggt act gca cgc ctt gct agt tta atg aat ctt gga 494
Arg Met Asn Gln Gly Thr Ala Arg Leu Ala Ser Leu Met Asn Leu Gly
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atg agt tct tca ttg aat caa caa gga gct cat agt gca ctg tct tct 542
Met Ser Ser Ser Leu Asn Gln Gln Gly Ala His Ser Ala Leu Ser Ser
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Ala Ser Thr Ser Ser His Asn Leu Gln Ser Ile Phe Asn Ile Gly Ser
80 85 90

aga ggt cca ctc cct tta tct tct caa cac cgt gga gat gca gac cag 638
Arg Gly Pro Leu Pro Leu Ser Ser Gln His Arg Gly Asp Ala Asp Gln
95 100 105

gcc agt aac att ttg gcc agc ttt ggt ctg tct gct aga gac tta gat 686
Ala Ser Asn Ile Leu Ala Ser Phe Gly Leu Ser Ala Arg Asp Leu Asp
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Glu Leu Ser Arg Tyr Pro Glu Asp Lys Ile Thr Pro Glu Asn Leu Pro
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Arg Val Pro Arg Asp Asp Trp Glu Glu Lys Arg His Phe Arg Arg Asp	
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Ser Phe Asp Asp Arg Gly Pro Ser Leu Asn Pro Val Leu Asp Tyr Asp	
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His Gly Ser Arg Ser Gln Glu Ser Gly Tyr Tyr Asp Arg Met Asp Tyr	
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Phe Gly Glu Thr Ser His Asn Tyr His Lys Phe Asp Ser Glu Tyr Glu	
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Lys Lys Arg Gly Ala Pro Pro Ser Ser Asn Ile Glu Asp Phe His Gly	
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His	Leu	Gly	Gly	Pro	Ala	Val	Gly	Pro	Arg	Gly	Asn	Leu	Gly	Ala	Gly	
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aat	gga	aac	ctg	caa	gga	cct	aga	cac	atg	cag	aaa	ggc	aga	gtg	gaa	1502
Asn	Gly	Asn	Leu	Gln	Gly	Pro	Arg	His	Met	Gln	Lys	Gly	Arg	Val	Glu	
380					385					390					395	
act	agc	aga	gtt	gtt	cac	atc	atg	gat	ttt	caa	cga	ggg	aaa	aac	ttg	1550
Thr	Ser	Arg	Val	Val	His	Ile	Met	Asp	Phe	Gln	Arg	Gly	Lys	Asn	Leu	
				400					405						410	
aga	tac	cag	cta	tta	cag	ctg	gta	gaa	cca	ttt	gga	gtc	att	tca	aat	1598
Arg	Tyr	Gln	Leu	Leu	Gln	Leu	Val	Glu	Pro	Phe	Gly	Val	Ile	Ser	Asn	
			415					420					425			
cat	ctg	att	cta	aat	aaa	att	aat	gag	gca	ttt	att	gaa	atg	gca	acc	1646
His	Leu	Ile	Leu	Asn	Lys	Ile	Asn	Glu	Ala	Phe	Ile	Glu	Met	Ala	Thr	
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Thr	Glu	Asp	Ala	Gln	Ala	Ala	Val	Asp	Tyr	Tyr	Thr	Thr	Thr	Pro	Ala	
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Arg	Ile	Lys	Lys	Pro	Glu	Gly	Lys	Pro	Asp	Gln	Lys	Phe	Asp	Gln	Lys	
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caa	gag	ctt	gga	cgt	gtg	ata	cat	ctc	agc	aat	ttg	ccg	cat	tct	ggc	1838
Gln	Glu	Leu	Gly	Arg	Val	Ile	His	Leu	Ser	Asn	Leu	Pro	His	Ser	Gly	
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Tyr	Ser	Asp	Ser	Ala	Val	Leu	Lys	Leu	Ala	Glu	Pro	Tyr	Gly	Lys	Ile	
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Lys	Asn	Tyr	Ile	Leu	Met	Arg	Met	Lys	Ser	Gln	Ala	Phe	Ile	Glu	Met	
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Glu	Thr	Arg	Glu	Asp	Ala	Met	Ala	Met	Val	Asp	His	Cys	Leu	Lys	Lys	
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Val Lys Lys Asp Gly Ser Ala Ser Ala Ala Lys Lys Lys Leu Lys	
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Ser Glu Asn Ala Asp Asp Pro Asn Lys Asp Thr Ser Glu Asn Ala Asp	
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Gly Gln Ser Asp Glu Asn Lys Asp Asp Tyr Thr Ile Pro Asp Glu Tyr	
765 770 775	
aga att gga cca tat cag ccc aat gtt cct gtt ggt ata gac tat gtg	2702
Arg Ile Gly Pro Tyr Gln Pro Asn Val Pro Val Gly Ile Asp Tyr Val	
780 785 790 795	
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Asn Glu Glu Val Ala Lys Asn Thr His Cys Ser Ser Leu Pro His Tyr	
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cag aaa tta aag aaa ttt ctg aat aaa ttg gca gaa gaa cgc aga cag	2846
Gln Lys Leu Lys Lys Phe Leu Asn Lys Leu Ala Glu Glu Arg Arg Gln	
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 35 40 45

Thr Ala Arg Leu Ala Ser Leu Met Asn Leu Gly Met Ser Ser Ser Leu
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Asn Gln Gln Gly Ala His Ser Ala Leu Ser Ser Ala Ser Thr Ser Ser
 65 70 75 80

His Asn Leu Gln Ser Ile Phe Asn Ile Gly Ser Arg Gly Pro Leu Pro
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Leu Ser Ser Gln His Arg Gly Asp Ala Asp Gln Ala Ser Asn Ile Leu
 100 105 110

Ala Ser Phe Gly Leu Ser Ala Arg Asp Leu Asp Glu Leu Ser Arg Tyr
 67/201

115		120		125
Pro Glu Asp Lys Ile Thr	Pro Glu Asn Leu Pro	Gln Ile Leu Leu Gln		
130	135	140		
Leu Lys Arg Arg Arg Thr	Glu Glu Gly Pro Thr	Leu Ser Tyr Gly Arg		
145	150	155		160
Asp Gly Arg Ser Ala Thr	Arg Glu Pro Pro Tyr	Arg Val Pro Arg Asp		
	165	170		175
Asp Trp Glu Glu Lys Arg His	Phe Arg Arg Asp Ser	Phe Asp Asp Arg		
	180	185		190
Gly Pro Ser Leu Asn Pro Val	Leu Asp Tyr Asp His	Gly Ser Arg Ser		
	195	200		205
Gln Glu Ser Gly Tyr Tyr	Asp Arg Met Asp Tyr	Glu Asp Asp Arg Leu		
	210	215		220
Arg Asp Gly Glu Arg Cys	Arg Asp Asp Ser Phe	Phe Gly Glu Thr Ser		
225	230	235		240
His Asn Tyr His Lys Phe	Asp Ser Glu Tyr Glu	Arg Met Gly Arg Gly		
	245	250		255
Pro Gly Pro Leu Gln Glu	Arg Ser Leu Phe Glu	Lys Lys Arg Gly Ala		
	260	265		270
Pro Pro Ser Ser Asn Ile	Glu Asp Phe His Gly	Leu Leu Pro Lys Gly		
	275	280		285
Tyr Pro His Leu Cys Ser	Ile Cys Asp Leu Pro	Val His Ser Asn Lys		
	290	295		300
Glu Trp Ser Gln His Ile	Asn Gly Ala Ser His	Ser Arg Arg Cys Gln		
305	310	315		320

Leu Leu Leu Glu Ile Tyr Pro Glu Trp Asn Pro Asp Asn Asp Thr Gly
325 330 335

His Thr Met Gly Asp Pro Phe Met Leu Gln Gln Ser Thr Asn Pro Ala
340 345 350

Pro Gly Ile Leu Gly Pro Pro Pro Ser Phe His Leu Gly Gly Pro
355 360 365

Ala Val Gly Pro Arg Gly Asn Leu Gly Ala Gly Asn Gly Asn Leu Gln
370 375 380

Gly Pro Arg His Met Gln Lys Gly Arg Val Glu Thr Ser Arg Val Val
385 390 395 400

His Ile Met Asp Phe Gln Arg Gly Lys Asn Leu Arg Tyr Gln Leu Leu
405 410 415

Gln Leu Val Glu Pro Phe Gly Val Ile Ser Asn His Leu Ile Leu Asn
420 425 430

Lys Ile Asn Glu Ala Phe Ile Glu Met Ala Thr Thr Glu Asp Ala Gln
435 440 445

Ala Ala Val Asp Tyr Tyr Thr Thr Thr Pro Ala Leu Val Phe Gly Lys
450 455 460

Pro Val Arg Val His Leu Ser Gln Lys Tyr Lys Arg Ile Lys Lys Pro
465 470 475 480

Glu Gly Lys Pro Asp Gln Lys Phe Asp Gln Lys Gln Glu Leu Gly Arg
485 490 495

Val Ile His Leu Ser Asn Leu Pro His Ser Gly Tyr Ser Asp Ser Ala
500 505 510

Val Leu Lys Leu Ala Glu Pro Tyr Gly Lys Ile Lys Asn Tyr Ile Leu
69/201

515					520					525					
Met	Arg	Met	Lys	Ser	Gln	Ala	Phe	Ile	Glu	Met	Glu	Thr	Arg	Glu	Asp
530						535					540				
Ala	Met	Ala	Met	Val	Asp	His	Cys	Leu	Lys	Lys	Ala	Leu	Trp	Phe	Gln
545					550					555					560
Gly	Arg	Cys	Val	Lys	Val	Asp	Leu	Ser	Glu	Lys	Tyr	Lys	Lys	Leu	Val
				565					570					575	
Leu	Arg	Ile	Pro	Asn	Arg	Gly	Ile	Asp	Leu	Leu	Lys	Lys	Asp	Lys	Ser
			580					585					590		
Arg	Lys	Arg	Ser	Tyr	Ser	Pro	Asp	Gly	Lys	Glu	Ser	Pro	Ser	Asp	Lys
		595					600					605			
Lys	Ser	Lys	Thr	Asp	Gly	Ser	Gln	Lys	Thr	Glu	Ser	Ser	Thr	Glu	Gly
610						615					620				
Lys	Glu	Gln	Glu	Glu	Lys	Ser	Gly	Glu	Asp	Gly	Glu	Lys	Asp	Thr	Lys
625					630					635					640
Asp	Asp	Gln	Thr	Glu	Gln	Glu	Pro	Asn	Met	Leu	Leu	Glu	Ser	Glu	Asp
				645					650					655	
Glu	Leu	Leu	Val	Asp	Glu	Glu	Glu	Ala	Ala	Ala	Leu	Leu	Glu	Ser	Gly
			660					665					670		
Ser	Ser	Val	Gly	Asp	Glu	Thr	Asp	Leu	Ala	Asn	Leu	Gly	Asp	Val	Ala
		675					680					685			
Ser	Asp	Gly	Lys	Lys	Glu	Pro	Ser	Asp	Lys	Ala	Val	Lys	Lys	Asp	Gly
690						695					700				
Ser	Ala	Ser	Ala	Ala	Ala	Lys	Lys	Lys	Leu	Lys	Lys	Val	Asp	Lys	Ile
705					710					715					720

Glu Glu Leu Asp Gln Glu Asn Glu Ala Ala Leu Glu Asn Gly Ile Lys
725 730 735

Asn Glu Glu Asn Thr Glu Pro Gly Ala Glu Ser Ser Glu Asn Ala Asp
740 745 750

Asp Pro Asn Lys Asp Thr Ser Glu Asn Ala Asp Gly Gln Ser Asp Glu
755 760 765

Asn Lys Asp Asp Tyr Thr Ile Pro Asp Glu Tyr Arg Ile Gly Pro Tyr
770 775 780

Gln Pro Asn Val Pro Val Gly Ile Asp Tyr Val Ile Pro Lys Thr Gly
785 790 795 800

Phe Tyr Cys Lys Leu Cys Ser Leu Phe Tyr Thr Asn Glu Glu Val Ala
805 810 815

Lys Asn Thr His Cys Ser Ser Leu Pro His Tyr Gln Lys Leu Lys Lys
820 825 830

Phe Leu Asn Lys Leu Ala Glu Glu Arg Arg Gln Lys Lys Glu Thr
835 840 845

<210> 23
<211> 1339
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (47).. (1018)
<223>

<400> 23
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Met Ala Ser
1

atc tgg gtt gga cac cga gga aca gta aga gat tat cca gac ttt agc 103
Ile Trp Val Gly His Arg Gly Thr Val Arg Asp Tyr Pro Asp Phe Ser
71/201

5	10	15	
cca tca gtg gat gct gaa gct att cag aaa gca atc aga gga att gga Pro Ser Val Asp Ala Glu Ala Ile Gln Lys Ala Ile Arg Gly Ile Gly 20 25 30 35			151
act gat gag aaa atg ctc atc agc att ctg act gag agg tca aat gca Thr Asp Glu Lys Met Leu Ile Ser Ile Leu Thr Glu Arg Ser Asn Ala 40 45 50			199
cag cgg cag ctg att gtt aag gaa tat caa gca gca tat gga aag gag Gln Arg Gln Leu Ile Val Lys Glu Tyr Gln Ala Ala Tyr Gly Lys Glu 55 60 65			247
ctg aaa gat gac ttg aag ggt gat ctc tct ggc cac ttt gag cat ctc Leu Lys Asp Asp Leu Lys Gly Asp Leu Ser Gly His Phe Glu His Leu 70 75 80			295
atg gtg gcc cta gtg act cca cca gca gtc ttt gat gca aag cag cta Met Val Ala Leu Val Thr Pro Pro Ala Val Phe Asp Ala Lys Gln Leu 85 90 95			343
aag aaa tcc atg aag ggc gcg gga aca aac gaa gat gcc ttg att gaa Lys Lys Ser Met Lys Gly Ala Gly Thr Asn Glu Asp Ala Leu Ile Glu 100 105 110 115			391
atc tta act acc agg aca agc agg caa atg aag gat atc tct caa gcc Ile Leu Thr Thr Arg Thr Ser Arg Gln Met Lys Asp Ile Ser Gln Ala 120 125 130			439
tat tat aca gta tac aag aag agt ctt gga gat gac att agt tcc gaa Tyr Tyr Thr Val Tyr Lys Lys Ser Leu Gly Asp Asp Ile Ser Ser Glu 135 140 145			487
aca tct ggt gac ttc cgg aaa gct ctg ttg act ttg gca gat ggc aga Thr Ser Gly Asp Phe Arg Lys Ala Leu Leu Thr Leu Ala Asp Gly Arg 150 155 160			535
aga gat gaa agt ctg aaa gtg gat gag cat ctg gcc aaa caa gat gcc Arg Asp Glu Ser Leu Lys Val Asp Glu His Leu Ala Lys Gln Asp Ala 165 170 175			583
cag att ctc tat aaa gct ggt gag aac aga tgg ggc acg gat gaa gac Gln Ile Leu Tyr Lys Ala Gly Glu Asn Arg Trp Gly Thr Asp Glu Asp 180 185 190 195			631
aaa ttc act gag atc ctg tgt tta agg agc ttt cct caa tta aaa cta Lys Phe Thr Glu Ile Leu Cys Leu Arg Ser Phe Pro Gln Leu Lys Leu 200 205 210			679

aca ttt gat gaa tac aga aat atc agc caa aag gac att gtg gac agc	727
Thr Phe Asp Glu Tyr Arg Asn Ile Ser Gln Lys Asp Ile Val Asp Ser	
215 220 225	
ata aaa gga gaa tta tct ggg cat ttt gaa gac tta ctg ttg gcc ata	775
Ile Lys Gly Glu Leu Ser Gly His Phe Glu Asp Leu Leu Leu Ala Ile	
230 235 240	
gtt aat tgt gtg agg aac acg ccg gcc ttt tta gcc gaa aga ctg cat	823
Val Asn Cys Val Arg Asn Thr Pro Ala Phe Leu Ala Glu Arg Leu His	
245 250 255	
cga gcc ttg aag ggt att gga act gat gag ttt act ctg aac cga ata	871
Arg Ala Leu Lys Gly Ile Gly Thr Asp Glu Phe Thr Leu Asn Arg Ile	
260 265 270 275	
atg gtg tcc aga tca gaa att gac ctt ttg gac att cga aca gag ttc	919
Met Val Ser Arg Ser Glu Ile Asp Leu Leu Asp Ile Arg Thr Glu Phe	
280 285 290	
aag aag cat tat ggc tat tcc cta tat tca gca att aaa tcg gat act	967
Lys Lys His Tyr Gly Tyr Ser Leu Tyr Ser Ala Ile Lys Ser Asp Thr	
295 300 305	
tct gga gac tat gaa atc aca ctc tta aaa atc tgt ggt gga gat gac	1015
Ser Gly Asp Tyr Glu Ile Thr Leu Leu Lys Ile Cys Gly Gly Asp Asp	
310 315 320	
tga accaagaaga taatctccaa aggtccacga tgggctttcc caacagctcc	1068
accttacttc ttctcatact atttaagaga acaagcaaata ataaacagca acttgtgttc	1128
ctaacaggaa ttttcattgt tctataacaa caacaacaaa agcgattatt attttagagc	1188
atctcattta taatgtagca gctcataaat gaaattgaaa atggtattaa agatctgcaa	1248
ctactatcca acttataattt ctgctttcaa agttaagaat ctttatagtt ctactccatt	1308
aaatataaag caagataata aaacggaatt c	1339

<210> 24
 <211> 323
 <212> PRT
 <213> Homo sapiens

<400> 24

Met	Ala	Ser	Ile	Trp	Val	Gly	His	Arg	Gly	Thr	Val	Arg	Asp	Tyr	Pro
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Asp Phe Ser Pro Ser Val Asp Ala Glu Ala Ile Gln Lys Ala Ile Arg
20 25 30

Gly Ile Gly Thr Asp Glu Lys Met Leu Ile Ser Ile Leu Thr Glu Arg
35 40 45

Ser Asn Ala Gln Arg Gln Leu Ile Val Lys Glu Tyr Gln Ala Ala Tyr
50 55 60

Gly Lys Glu Leu Lys Asp Asp Leu Lys Gly Asp Leu Ser Gly His Phe
65 70 75 80

Glu His Leu Met Val Ala Leu Val Thr Pro Pro Ala Val Phe Asp Ala
85 90 95

Lys Gln Leu Lys Lys Ser Met Lys Gly Ala Gly Thr Asn Glu Asp Ala
100 105 110

Leu Ile Glu Ile Leu Thr Thr Arg Thr Ser Arg Gln Met Lys Asp Ile
115 120 125

Ser Gln Ala Tyr Tyr Thr Val Tyr Lys Lys Ser Leu Gly Asp Asp Ile
130 135 140

Ser Ser Glu Thr Ser Gly Asp Phe Arg Lys Ala Leu Leu Thr Leu Ala
145 150 155 160

Asp Gly Arg Arg Asp Glu Ser Leu Lys Val Asp Glu His Leu Ala Lys
165 170 175

Gln Asp Ala Gln Ile Leu Tyr Lys Ala Gly Glu Asn Arg Trp Gly Thr
180 185 190

Asp Glu Asp Lys Phe Thr Glu Ile Leu Cys Leu Arg Ser Phe Pro Gln
195 200 205

Leu Lys Leu Thr Phe Asp Glu Tyr Arg Asn Ile Ser Gln Lys Asp Ile
 210 215 220

Val Asp Ser Ile Lys Gly Glu Leu Ser Gly His Phe Glu Asp Leu Leu
 225 230 235 240

Leu Ala Ile Val Asn Cys Val Arg Asn Thr Pro Ala Phe Leu Ala Glu
 245 250 255

Arg Leu His Arg Ala Leu Lys Gly Ile Gly Thr Asp Glu Phe Thr Leu
 260 265 270

Asn Arg Ile Met Val Ser Arg Ser Glu Ile Asp Leu Leu Asp Ile Arg
 275 280 285

Thr Glu Phe Lys Lys His Tyr Gly Tyr Ser Leu Tyr Ser Ala Ile Lys
 290 295 300

Ser Asp Thr Ser Gly Asp Tyr Glu Ile Thr Leu Leu Lys Ile Cys Gly
 305 310 315 320

Gly Asp Asp

<210> 25
 <211> 1659
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (152).. (1201)
 <223>

<400> 25
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 acatcctcca cctctcttgg tccagcgagc gttgccgggc cagggtcaag cggagggctc 120
 cgacggcgcg gacggagcga agcgccgagc c atg gcg cac caa acg ggc atc 172
 Met Ala His Gln Thr Gly Ile
 1 5

cac gcc acg gaa gag ctg aag gaa ttc ttt gcc aag gca cgg gct ggc His Ala Thr Glu Glu Leu Lys Glu Phe Phe Ala Lys Ala Arg Ala Gly 10 15 20	220
tct gtg cgg ctc atc aag gtt gtg att gag gac gag cag ctc gtg ctg Ser Val Arg Leu Ile Lys Val Val Ile Glu Asp Glu Gln Leu Val Leu 25 30 35	268
ggt gcc tcg cag gag cca gta ggc cgc tgg gat cag gac tat gac agg Gly Ala Ser Gln Glu Pro Val Gly Arg Trp Asp Gln Asp Tyr Asp Arg 40 45 50 55	316
gcc gtg ctg cca ctg ctg gac gcc cag cag ccc tgc tac ctg ctc tac Ala Val Leu Pro Leu Leu Asp Ala Gln Gln Pro Cys Tyr Leu Leu Tyr 60 65 70	364
cgc ctc gac tca cag aat gct cag ggc ttc gaa tgg ctc ttc ctc gcc Arg Leu Asp Ser Gln Asn Ala Gln Gly Phe Glu Trp Leu Phe Leu Ala 75 80 85	412
tgg tcg cct gat aac tcc ccc gtg cgg ctg aag atg ctg tac gcg gcc Trp Ser Pro Asp Asn Ser Pro Val Arg Leu Lys Met Leu Tyr Ala Ala 90 95 100	460
acg cgg gcc aca gtg aaa aag gag ttt gga ggt ggc cac atc aag gat Thr Arg Ala Thr Val Lys Lys Glu Phe Gly Gly Gly His Ile Lys Asp 105 110 115	508
gag ctc ttc ggg act gtg aag gat gac ctc tct ttt gct ggg tac cag Glu Leu Phe Gly Thr Val Lys Asp Asp Leu Ser Phe Ala Gly Tyr Gln 120 125 130 135	556
aaa cac ctg tcg tcc tgt gcg gca cct gcc ccg ctg acc tcg gct gag Lys His Leu Ser Ser Cys Ala Ala Pro Ala Pro Leu Thr Ser Ala Glu 140 145 150	604
aga gag ctc cag cag atc cgc att aac gag gtg aag aca gag atc agt Arg Glu Leu Gln Gln Ile Arg Ile Asn Glu Val Lys Thr Glu Ile Ser 155 160 165	652
gtg gaa agc aag cac cag acc ctg cag ggc ctc gcc ttc ccc ctg cag Val Glu Ser Lys His Gln Thr Leu Gln Gly Leu Ala Phe Pro Leu Gln 170 175 180	700
cct gag gcc cag cgg gca ctc cag cag ctc aag cag aaa atg gtc aac Pro Glu Ala Gln Arg Ala Leu Gln Gln Leu Lys Gln Lys Met Val Asn 185 190 195	748
tac atc cag atg aag ctg gac cta gag cgg gaa acc att gag ctg gtg	796

Tyr	Ile	Gln	Met	Lys	Leu	Asp	Leu	Glu	Arg	Glu	Thr	Ile	Glu	Leu	Val	
200					205					210					215	
cac	aca	gag	ccc	acg	gat	gtg	gcc	cag	ctg	ccc	tcc	cgg	gtg	ccc	cga	844
His	Thr	Glu	Pro	Thr	Asp	Val	Ala	Gln	Leu	Pro	Ser	Arg	Val	Pro	Arg	
				220					225					230		
gat	gct	gcc	cgc	tac	cac	ttc	ttc	ctc	tac	aag	cac	acc	cat	gag	ggc	892
Asp	Ala	Ala	Arg	Tyr	His	Phe	Phe	Leu	Tyr	Lys	His	Thr	His	Glu	Gly	
			235					240					245			
gac	ccc	ctt	gag	tct	gta	gtg	ttc	atc	tac	tcc	atg	ccg	ggg	tac	aag	940
Asp	Pro	Leu	Glu	Ser	Val	Val	Phe	Ile	Tyr	Ser	Met	Pro	Gly	Tyr	Lys	
		250					255					260				
tgc	agc	atc	aag	gag	cga	atg	ctc	tac	tcc	agc	tgc	aag	agc	cgc	ctc	988
Cys	Ser	Ile	Lys	Glu	Arg	Met	Leu	Tyr	Ser	Ser	Cys	Lys	Ser	Arg	Leu	
	265					270					275					
ctc	gac	tcc	gtg	gag	cag	gac	ttc	cat	ctg	gag	atc	gcc	aag	aaa	att	1036
Leu	Asp	Ser	Val	Glu	Gln	Asp	Phe	His	Leu	Glu	Ile	Ala	Lys	Lys	Ile	
280					285					290					295	
gag	att	ggc	gat	ggg	gca	gag	ctg	acg	gca	gag	ttc	ctc	tac	gac	gag	1084
Glu	Ile	Gly	Asp	Gly	Ala	Glu	Leu	Thr	Ala	Glu	Phe	Leu	Tyr	Asp	Glu	
				300					305					310		
gtg	cac	ccc	aag	caa	cac	gcc	ttc	aag	cag	gcc	ttc	gcc	aag	ccc	aag	1132
Val	His	Pro	Lys	Gln	His	Ala	Phe	Lys	Gln	Ala	Phe	Ala	Lys	Pro	Lys	
			315					320				325				
ggc	cca	ggg	ggc	aag	cgg	ggc	cat	aag	cgc	ctc	atc	cgc	ggc	ccg	ggt	1180
Gly	Pro	Gly	Gly	Lys	Arg	Gly	His	Lys	Arg	Leu	Ile	Arg	Gly	Pro	Gly	
		330					335				340					
gaa	aat	ggg	gat	gac	agc	tag	gaggctggag	cagggccggc	cacgtgtgga							1231
Glu	Asn	Gly	Asp	Asp	Ser											
	345															
ctgtggggct	gcccaccttc	cgctccctgc	caccatcctc	cttcctgggc	tccaggaaag											1291
tgtttctggg	aggtcaggag	ggctggcagc	tgaacgcact	tgcagcgtcc	gagggccacc											1351
gggctggcat	tttgtgaccc	ttccctgttg	ctgtccctgc	atctcgtctg	tgtgcccagg											1411
gtgtccgggg	accctgcctg	gctggcttaa	gggggctggg	tcaggggcct	ggcatgaacc											1471
tggcctcccg	gggagctgag	actaggggtcc	cagcacagcc	cagaaacctt	tggccacaag											1531
aagtggggtc	agtcagggtc	ggggcagggg	tcaactgcagt	ttgggatggt	tgaatgctgt											1591

attttctaaa gaataaaata ttttttaaadc aagaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1651
aaaaaaaaa 1659

<210> 26
<211> 349
<212> PRT
<213> Homo sapiens

<400> 26

Met Ala His Gln Thr Gly Ile His Ala Thr Glu Glu Leu Lys Glu Phe
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Phe Ala Lys Ala Arg Ala Gly Ser Val Arg Leu Ile Lys Val Val Ile
20 25 30

Glu Asp Glu Gln Leu Val Leu Gly Ala Ser Gln Glu Pro Val Gly Arg
35 40 45

Trp Asp Gln Asp Tyr Asp Arg Ala Val Leu Pro Leu Leu Asp Ala Gln
50 55 60

Gln Pro Cys Tyr Leu Leu Tyr Arg Leu Asp Ser Gln Asn Ala Gln Gly
65 70 75 80

Phe Glu Trp Leu Phe Leu Ala Trp Ser Pro Asp Asn Ser Pro Val Arg
85 90 95

Leu Lys Met Leu Tyr Ala Ala Thr Arg Ala Thr Val Lys Lys Glu Phe
100 105 110

Gly Gly Gly His Ile Lys Asp Glu Leu Phe Gly Thr Val Lys Asp Asp
115 120 125

Leu Ser Phe Ala Gly Tyr Gln Lys His Leu Ser Ser Cys Ala Ala Pro
130 135 140

Ala Pro Leu Thr Ser Ala Glu Arg Glu Leu Gln Gln Ile Arg Ile Asn
78/201

145		150		155		160
Glu Val Lys Thr	Glu Ile Ser Val	Glu Ser Lys His	Gln Thr Leu Gln			
	165		170			175
Gly Leu Ala Phe	Pro Leu Gln Pro	Glu Ala Gln Arg	Ala Leu Gln Gln			
	180		185			190
Leu Lys Gln Lys	Met Val Asn Tyr	Ile Gln Met Lys	Leu Asp Leu Glu			
	195		200			205
Arg Glu Thr Ile	Glu Leu Val His	Thr Glu Pro Thr	Asp Val Ala Gln			
	210		215			220
Leu Pro Ser Arg	Val Pro Arg Asp	Ala Ala Arg Tyr	His Phe Phe Leu			
	225		230			235
Tyr Lys His Thr	His Glu Gly Asp	Pro Leu Glu Ser	Val Val Phe Ile			
	245		250			255
Tyr Ser Met Pro	Gly Tyr Lys Cys	Ser Ile Lys Glu	Arg Met Leu Tyr			
	260		265			270
Ser Ser Cys Lys	Ser Arg Leu Leu	Asp Ser Val Glu	Gln Asp Phe His			
	275		280			285
Leu Glu Ile Ala	Lys Lys Ile Glu	Ile Gly Asp Gly	Ala Glu Leu Thr			
	290		295			300
Ala Glu Phe Leu	Tyr Asp Glu Val	His Pro Lys Gln	His Ala Phe Lys			
	305		310			315
Gln Ala Phe Ala	Lys Pro Lys Gly	Pro Gly Gly Lys	Arg Gly His Lys			
	325		330			335
Arg Leu Ile Arg	Gly Pro Gly Glu	Asn Gly Asp Asp	Ser			
	340		345			

<210> 27
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 <212> DNA
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<220>
 <221> CDS
 <222> (91)..(837)
 <223>

<400> 27

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gttctcgagt ccgcgctttt cgtcaccgcc atg tcg gga ggt ggt gtg att cgt	114
Met Ser Gly Gly Gly Val Ile Arg	
1 5	
ggc ccc gca ggg aac aac gat tgc cgc atc tac gtg ggt aac tta cct	162
Gly Pro Ala Gly Asn Asn Asp Cys Arg Ile Tyr Val Gly Asn Leu Pro	
10 15 20	
cca gac atc cga acc aag gac att gag gac gtg ttc tac aaa tac ggc	210
Pro Asp Ile Arg Thr Lys Asp Ile Glu Asp Val Phe Tyr Lys Tyr Gly	
25 30 35 40	
gct atc cgc gac atc gac ctc aag aat cgc cgc ggg gga ccg ccc ttc	258
Ala Ile Arg Asp Ile Asp Leu Lys Asn Arg Arg Gly Gly Pro Pro Phe	
45 50 55	
gcc ttc gtt gag ttc gag gac ccg cga gac gcg gaa gac gcg gtg tat	306
Ala Phe Val Glu Phe Glu Asp Pro Arg Asp Ala Glu Asp Ala Val Tyr	
60 65 70	
ggt cgc gac ggc tat gat tac gat ggg tac cgt ctg cgg gtg gag ttt	354
Gly Arg Asp Gly Tyr Asp Tyr Asp Gly Tyr Arg Leu Arg Val Glu Phe	
75 80 85	
cct cga agc ggc cgt gga aca ggc cga ggc ggc ggc ggg ggt gga ggt	402
Pro Arg Ser Gly Arg Gly Thr Gly Arg Gly Gly Gly Gly Gly Gly Gly	
90 95 100	
ggc gga gct ccc cga ggt cgc tat ggc ccc cca tcc agg cgg tct gaa	450
Gly Gly Ala Pro Arg Gly Arg Tyr Gly Pro Pro Ser Arg Arg Ser Glu	
105 110 115 120	
aac aga gtg gtt gtc tct gga ctg cct cca agt gga agt tgg cag gat	498
Asn Arg Val Val Val Ser Gly Leu Pro Pro Ser Gly Ser Trp Gln Asp	
125 130 135	

tta aag gat cac atg cgt gaa gca ggt gat gta tgt tat gct gat gtt Leu Lys Asp His Met Arg Glu Ala Gly Asp Val Cys Tyr Ala Asp Val 140 145 150	546
tac cga gat ggc act ggt gtc gtg gag ttt gta cgg aaa gaa gat atg Tyr Arg Asp Gly Thr Gly Val Val Glu Phe Val Arg Lys Glu Asp Met 155 160 165	594
acc tat gca gtt cga aaa ctg gat aac act aag ttt aga tct cat gag Thr Tyr Ala Val Arg Lys Leu Asp Asn Thr Lys Phe Arg Ser His Glu 170 175 180	642
gga gaa act gcc tac atc cgg gtt aaa gtt gat ggg ccc aga agt cca Gly Glu Thr Ala Tyr Ile Arg Val Lys Val Asp Gly Pro Arg Ser Pro 185 190 195 200	690
agt tat gga aga tct cga tct cga agc cgt agt cgt agc aga agc cgt Ser Tyr Gly Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg 205 210 215	738
agc aga agc aac agc agg agt cgc agt tac tcc cca agg aga agc aga Ser Arg Ser Asn Ser Arg Ser Arg Ser Tyr Ser Pro Arg Arg Ser Arg 220 225 230	786
gga tca cca cgc tat tct ccc cgt cat agc aga tct cgc tct cgt aca Gly Ser Pro Arg Tyr Ser Pro Arg His Ser Arg Ser Arg Ser Arg Thr 235 240 245	834
taa gatgattggt gacacttttt gtagaaccca tggtgtatac agttttcctt	887
tattcagtac aatctttttca ttttttaatt caaactgttt tgttcagaat gggctaaagt	947
gttgaattgc attcttgtaa tatecccttg ctectaacaat ctacattccc ttcgtgtcctt	1007
tgataaattg tattttaagt gatgtcatag acaggattgt ttaaatttag ttaactccat	1067
actcttcaga ctgtgatatt gtgtaaatgt ctatctgccc tggtttgtgt gaactgggat	1127
gttgggggtg tttgtggta tcttacctgg ggaagttcct atgtttatct tgcttttcat	1187
gtgtctttct gtagacatat ctgaagagat ggattaagaa tgctttggat taaggattgt	1247
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aatggaggca atggtatgac tccaagtgtc attgtcacag atgaaattgg cagtattgac	1367
cttatactaa aaggcagggg ttaaaaatga ttatatacat tttccttaaa acacttgcaa	1427
acattttatt cagttgtcct tagctacaat tgctttgctt tttaaaccct ggcaattgtg	1487

gcaaaattat attgcccatt ttgtagcaac ttattttgct cccttcccc catttttggt	1547
ttaataggga ctaatgtggg aagaactggc taatttgtca cagtgccttag ttacaactgt	1607
taatgtgtga cctgctgttg gtgtacatgt gggtagagg tgtttttaaa tccaacaaga	1667
tagagtataa tatcaatact gctaaatctg catgtcctct gtgtgactga tagagcgttg	1727
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gataatctag ttgggaatac ttttaagtct caccttcccc tttaaactaa tattcataat	1847
tggttcatat gtttaaaaga ctttaattta caaattaaat tgcaaatggg agcattagat	1907
ttagtttttag acttaggtgg gtagcaatgc cagtaaactt aaattacgta acttcttgca	1967
accacgaaac ctgtaatacg ctgtacagta acaagtgttg gcattatcag ttgaactgta	2027
aatacaaaat gcttcttcca attagtctct atgatgatta agtttctaaa atttatctga	2087
acaccattca gaaacttggt ttggggaatt tgatagttat tgatgtgcat ctgttaaact	2147
gatgacagac ataactcatc attccccaga aacctttttt gattacagta tctaacttt	2207
tgctcctct tttttggttt tgctggttat aaaggtttg attggagagg gctcactgga	2267
tccaatcct tggagctgga tcattggatt caaatcataa tgtggatagg atagggagga	2327
tgaattacc aggattcatg gagcgggatc agattaccag gaacatagga gtggattcct	2387
gccccacca aaccgcattc gtgtggattt ttttattcaa cttaattggc tattccaaag	2447
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tgcgtttttt ggtaaaagga gcaaagcgag gacctggaga taaacgctgg agcaatctcc	2567
ttggaaggat tcagcacgag tagatggtaa acatttaaag gggaaagggg gggtttggtt	2627
aaaatagtaa atcagtaagt cacttctaaa tttaaagaaa aaaaattgg agttgaagaa	2687
taagtaggtt tccaattggc tattgcccgtt ttctttgaaa aaataaacat tttttaaaaa	2747
actaaaaaaaa aaaaaaaaa	2765

<210> 28
 <211> 248
 <212> PRT
 <213> Homo sapiens

<400> 28

Met Ser Gly Gly Gly Val Ile Arg Gly Pro Ala Gly Asn Asn Asp Cys
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Arg Ile Tyr Val Gly Asn Leu Pro Pro Asp Ile Arg Thr Lys Asp Ile
20 25 30

Glu Asp Val Phe Tyr Lys Tyr Gly Ala Ile Arg Asp Ile Asp Leu Lys
35 40 45

Asn Arg Arg Gly Gly Pro Pro Phe Ala Phe Val Glu Phe Glu Asp Pro
50 55 60

Arg Asp Ala Glu Asp Ala Val Tyr Gly Arg Asp Gly Tyr Asp Tyr Asp
65 70 75 80

Gly Tyr Arg Leu Arg Val Glu Phe Pro Arg Ser Gly Arg Gly Thr Gly
85 90 95

Arg Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Arg Gly Arg Tyr
100 105 110

Gly Pro Pro Ser Arg Arg Ser Glu Asn Arg Val Val Val Ser Gly Leu
115 120 125

Pro Pro Ser Gly Ser Trp Gln Asp Leu Lys Asp His Met Arg Glu Ala
130 135 140

Gly Asp Val Cys Tyr Ala Asp Val Tyr Arg Asp Gly Thr Gly Val Val
145 150 155 160

Glu Phe Val Arg Lys Glu Asp Met Thr Tyr Ala Val Arg Lys Leu Asp
165 170 175

Asn Thr Lys Phe Arg Ser His Glu Gly Glu Thr Ala Tyr Ile Arg Val
180 185 190

Lys Val Asp Gly Pro Arg Ser Pro Ser Tyr Gly Arg Ser Arg Ser Arg
195 200 205

Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Asn Ser Arg Ser Arg
210 215 220

Ser Tyr Ser Pro Arg Arg Ser Arg Gly Ser Pro Arg Tyr Ser Pro Arg
225 230 235 240

His Ser Arg Ser Arg Ser Arg Thr
245

<210> 29
<211> 1167
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (73)..(966)
<223>

<400> 29
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agagctgaag cc atg gtt cat cag gtg ctc tac cgg gcg ctg gtc tcc acc 111
Met Val His Gln Val Leu Tyr Arg Ala Leu Val Ser Thr
1 5 10
aag tgg ctg gcg gag tcc atc agg act ggc aag ctg ggg ccc ggc ctg 159
Lys Trp Leu Ala Glu Ser Ile Arg Thr Gly Lys Leu Gly Pro Gly Leu
15 20 25
cgg gtg ctg gac gcg tcc tgg tac tca cca ggc acc cga gag gcc cgc 207
Arg Val Leu Asp Ala Ser Trp Tyr Ser Pro Gly Thr Arg Glu Ala Arg
30 35 40 45
aag gag tac ctc gag cgc cac gta ccc ggc gcc tct ttc ttt gac ata 255
Lys Glu Tyr Leu Glu Arg His Val Pro Gly Ala Ser Phe Phe Asp Ile
50 55 60
gaa gag tgc cgg gac acg gcg tcg ccc tac gag atg atg ctg ccc agc 303
Glu Glu Cys Arg Asp Thr Ala Ser Pro Tyr Glu Met Met Leu Pro Ser
65 70 75
gag gct ggc ttc gcc gag tat gtg ggc cgc ctg ggc atc agc aac cac 351

Glu	Ala	Gly	Phe	Ala	Glu	Tyr	Val	Gly	Arg	Leu	Gly	Ile	Ser	Asn	His	
		80					85					90				
acg	cac	gtg	gtg	gtg	tat	gat	ggt	gaa	cac	ctg	ggc	agc	ttc	tat	gct	399
Thr	His	Val	Val	Val	Tyr	Asp	Gly	Glu	His	Leu	Gly	Ser	Phe	Tyr	Ala	
	95					100					105					
ccc	cgg	gtc	tgg	tgg	atg	ttc	cgt	gtg	ttt	ggc	cac	cgc	acc	gta	tca	447
Pro	Arg	Val	Trp	Trp	Met	Phe	Arg	Val	Phe	Gly	His	Arg	Thr	Val	Ser	
110					115					120					125	
gtg	ctc	aat	ggt	ggc	ttc	cgg	aac	tgg	ctg	aag	gag	ggc	cac	ccg	gtg	495
Val	Leu	Asn	Gly	Gly	Phe	Arg	Asn	Trp	Leu	Lys	Glu	Gly	His	Pro	Val	
				130					135					140		
aca	tcc	gag	ccc	tca	cgc	cca	gaa	ccg	gcc	gtc	ttc	aaa	gcc	aca	ctg	543
Thr	Ser	Glu	Pro	Ser	Arg	Pro	Glu	Pro	Ala	Val	Phe	Lys	Ala	Thr	Leu	
			145					150					155			
gac	cgc	tcc	ctg	ctc	aag	acc	tac	gag	cag	gtg	ctg	gag	aac	ctt	gaa	591
Asp	Arg	Ser	Leu	Leu	Lys	Thr	Tyr	Glu	Gln	Val	Leu	Glu	Asn	Leu	Glu	
		160					165					170				
tct	aag	agg	ttc	cag	ctg	gtg	gat	tca	agg	tct	caa	ggg	cgg	ttc	ctg	639
Ser	Lys	Arg	Phe	Gln	Leu	Val	Asp	Ser	Arg	Ser	Gln	Gly	Arg	Phe	Leu	
	175					180					185					
ggc	acc	gag	ccg	gag	ccg	gat	gca	gta	gga	ctg	gac	tcg	ggc	cat	atc	687
Gly	Thr	Glu	Pro	Glu	Pro	Asp	Ala	Val	Gly	Leu	Asp	Ser	Gly	His	Ile	
190					195					200					205	
cgt	ggt	gcc	gtc	aac	atg	cct	ttc	atg	gac	ttc	ctg	act	gag	gat	ggc	735
Arg	Gly	Ala	Val	Asn	Met	Pro	Phe	Met	Asp	Phe	Leu	Thr	Glu	Asp	Gly	
				210				215						220		
ttc	gag	aag	ggc	cca	gaa	gag	ctc	cgt	gct	ctg	ttc	cag	acc	aag	aag	783
Phe	Glu	Lys	Gly	Pro	Glu	Glu	Leu	Arg	Ala	Leu	Phe	Gln	Thr	Lys	Lys	
			225					230					235			
gtg	gat	ctc	tcg	cag	cct	ctc	att	gcc	acg	tgc	cgc	aag	gga	gtc	acc	831
Val	Asp	Leu	Ser	Gln	Pro	Leu	Ile	Ala	Thr	Cys	Arg	Lys	Gly	Val	Thr	
		240					245					250				
gcc	tgc	cac	gtg	gcc	ttg	gct	gcc	tac	ctc	tgc	ggc	aag	cct	gat	gtg	879
Ala	Cys	His	Val	Ala	Leu	Ala	Ala	Tyr	Leu	Cys	Gly	Lys	Pro	Asp	Val	
	255					260					265					
gcc	gtg	tac	gat	ggc	tcc	tgg	tcc	gag	tgg	ttt	cgc	cgg	gcc	ccc	cca	927
Ala	Val	Tyr	Asp	Gly	Ser	Trp	Ser	Glu	Trp	Phe	Arg	Arg	Ala	Pro	Pro	
270					275					280					285	

gag agc cgt gtg tcc cag gga aag tct gag aag gcc tga gccgtgacct 976
 Glu Ser Arg Val Ser Gln Gly Lys Ser Glu Lys Ala
 290 295

cttctgctta ctgtaactgc ggccgggttta gtgaccccat gacttacagc cggttcttac 1036

ctcttaggtg aaggagatga catgttttta gaattgctgt gcaaggctca ccctctctct 1096

gtcaacactg gaataaactt tgccttttct gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1156

aaaaaaaaaa a 1167

<210> 30
 <211> 297
 <212> PRT
 <213> Homo sapiens

<400> 30

Met Val His Gln Val Leu Tyr Arg Ala Leu Val Ser Thr Lys Trp Leu
 1 5 10 15

Ala Glu Ser Ile Arg Thr Gly Lys Leu Gly Pro Gly Leu Arg Val Leu
 20 25 30

Asp Ala Ser Trp Tyr Ser Pro Gly Thr Arg Glu Ala Arg Lys Glu Tyr
 35 40 45

Leu Glu Arg His Val Pro Gly Ala Ser Phe Phe Asp Ile Glu Glu Cys
 50 55 60

Arg Asp Thr Ala Ser Pro Tyr Glu Met Met Leu Pro Ser Glu Ala Gly
 65 70 75 80

Phe Ala Glu Tyr Val Gly Arg Leu Gly Ile Ser Asn His Thr His Val
 85 90 95

Val Val Tyr Asp Gly Glu His Leu Gly Ser Phe Tyr Ala Pro Arg Val
 100 105 110

Trp Trp Met Phe Arg Val Phe Gly His Arg Thr Val Ser Val Leu Asn
 86/201

115		120		125
Gly Gly Phe Arg Asn Trp Leu Lys Glu Gly His Pro Val Thr Ser Glu				
130		135		140
Pro Ser Arg Pro Glu Pro Ala Val Phe Lys Ala Thr Leu Asp Arg Ser				
145		150		155 160
Leu Leu Lys Thr Tyr Glu Gln Val Leu Glu Asn Leu Glu Ser Lys Arg				
		165		170 175
Phe Gln Leu Val Asp Ser Arg Ser Gln Gly Arg Phe Leu Gly Thr Glu				
		180		185 190
Pro Glu Pro Asp Ala Val Gly Leu Asp Ser Gly His Ile Arg Gly Ala				
		195		200 205
Val Asn Met Pro Phe Met Asp Phe Leu Thr Glu Asp Gly Phe Glu Lys				
		210		215 220
Gly Pro Glu Glu Leu Arg Ala Leu Phe Gln Thr Lys Lys Val Asp Leu				
225		230		235 240
Ser Gln Pro Leu Ile Ala Thr Cys Arg Lys Gly Val Thr Ala Cys His				
		245		250 255
Val Ala Leu Ala Ala Tyr Leu Cys Gly Lys Pro Asp Val Ala Val Tyr				
		260		265 270
Asp Gly Ser Trp Ser Glu Trp Phe Arg Arg Ala Pro Pro Glu Ser Arg				
		275		280 285
Val Ser Gln Gly Lys Ser Glu Lys Ala				
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<210> 31
 <211> 2110
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (48)..(1346)

<223>

<400> 31

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Met Ser Asp	
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aaa ctg ccc tac aaa gtc gcc gac atc ggc ctg gct gcc tgg gga cgc	104
Lys Leu Pro Tyr Lys Val Ala Asp Ile Gly Leu Ala Ala Trp Gly Arg	
5 10 15	

aag gcc ctg gac att gct gag aac gag atg ccg ggc ctg atg cgt atg	152
Lys Ala Leu Asp Ile Ala Glu Asn Glu Met Pro Gly Leu Met Arg Met	
20 25 30 35	

cgg gag cgg tac tcg gcc tcc aag cca ctg aag ggc gcc cgc atc gct	200
Arg Glu Arg Tyr Ser Ala Ser Lys Pro Leu Lys Gly Ala Arg Ile Ala	
40 45 50	

ggc tgc ctg cac atg acc gtg gag acg gcc gtc ctc att gag acc ctc	248
Gly Cys Leu His Met Thr Val Glu Thr Ala Val Leu Ile Glu Thr Leu	
55 60 65	

gtc acc ctg ggt gct gag gtg cag tgg tcc agc tgc aac atc ttc tcc	296
Val Thr Leu Gly Ala Glu Val Gln Trp Ser Ser Cys Asn Ile Phe Ser	
70 75 80	

acc cag gac cat gcg gcg gct gcc att gcc aag gct ggc att ccg gtg	344
Thr Gln Asp His Ala Ala Ala Ala Ile Ala Lys Ala Gly Ile Pro Val	
85 90 95	

tat gcc tgg aag ggc gaa acg gac gag gag tac ctg tgg tgc att gag	392
Tyr Ala Trp Lys Gly Glu Thr Asp Glu Glu Tyr Leu Trp Cys Ile Glu	
100 105 110 115	

cag acc ctg tac ttc aag gac ggg ccc ctc aac atg att ctg gac gac	440
Gln Thr Leu Tyr Phe Lys Asp Gly Pro Leu Asn Met Ile Leu Asp Asp	
120 125 130	

ggg ggc gac ctc acc aac ctc atc cac acc aag tac ccg cag ctt ctg	488
Gly Gly Asp Leu Thr Asn Leu Ile His Thr Lys Tyr Pro Gln Leu Leu	
135 140 145	

cca ggc atc cga ggc atc tct gag gag acc acg act ggg gtc cac aac	536
Pro Gly Ile Arg Gly Ile Ser Glu Glu Thr Thr Thr Gly Val His Asn	

150	155	160	
ctc tac aag atg atg gcc aat ggg atc ctc aag gtg cct gcc atc aat Leu Tyr Lys Met Met Ala Asn Gly Ile Leu Lys Val Pro Ala Ile Asn 165 170 175			584
gtc aat gac tcc gtc acc aag agc aag ttt gac aac ctc tat ggc tgc Val Asn Asp Ser Val Thr Lys Ser Lys Phe Asp Asn Leu Tyr Gly Cys 180 185 190 195			632
cgg gag tcc ctc ata gat ggc atc aag cgg gcc aca gat gtg atg att Arg Glu Ser Leu Ile Asp Gly Ile Lys Arg Ala Thr Asp Val Met Ile 200 205 210			680
gcc ggc aag gta gcg gtg gta gca ggc tat ggt gat gtg ggc aag ggc Ala Gly Lys Val Ala Val Val Ala Gly Tyr Gly Asp Val Gly Lys Gly 215 220 225			728
tgt gcc cag gcc ctg cgg ggt ttc gga gcc cgc gtc atc atc acc gag Cys Ala Gln Ala Leu Arg Gly Phe Gly Ala Arg Val Ile Ile Thr Glu 230 235 240			776
att gac ccc atc aac gca ctg cag gct gcc atg gag ggc tat gag gtg Ile Asp Pro Ile Asn Ala Leu Gln Ala Ala Met Glu Gly Tyr Glu Val 245 250 255			824
acc acc atg gat gag gcc tgt cag gag ggc aac atc ttt gtc acc acc Thr Thr Met Asp Glu Ala Cys Gln Glu Gly Asn Ile Phe Val Thr Thr 260 265 270 275			872
aca ggc tgt att gac atc atc ctt ggc cgg cac ttt gag cag atg aag Thr Gly Cys Ile Asp Ile Ile Leu Gly Arg His Phe Glu Gln Met Lys 280 285 290			920
gat gat gcc att gtg tgt aac att gga cac ttt gac gtg gag atc gat Asp Asp Ala Ile Val Cys Asn Ile Gly His Phe Asp Val Glu Ile Asp 295 300 305			968
gtc aag tgg ctc aac gag aac gcc gtg gag aag gtg aac atc aag ccg Val Lys Trp Leu Asn Glu Asn Ala Val Glu Lys Val Asn Ile Lys Pro 310 315 320			1016
cag gtg gac cgg tat cgg ttg aag aat ggg cgc cgc atc atc ctg ctg Gln Val Asp Arg Tyr Arg Leu Lys Asn Gly Arg Arg Ile Ile Leu Leu 325 330 335			1064
gcc gag ggt cgg ctg gtc aac ctg ggt tgt gcc atg ggc cac ccc agc Ala Glu Gly Arg Leu Val Asn Leu Gly Cys Ala Met Gly His Pro Ser 340 345 350 355			1112

ttc gtg atg agt aac tcc ttc acc aac cag gtg atg gcg cag atc gag	1160
Phe Val Met Ser Asn Ser Phe Thr Asn Gln Val Met Ala Gln Ile Glu	
360 365 370	
ctg tgg acc cat cca gac aag tac ccc gtt ggg gtt cat ttc ctg ccc	1208
Leu Trp Thr His Pro Asp Lys Tyr Pro Val Gly Val His Phe Leu Pro	
375 380 385	
aag aag ctg gat gag gca gtg gct gaa gcc cac ctg ggc aag ctg aat	1256
Lys Lys Leu Asp Glu Ala Val Ala Glu Ala His Leu Gly Lys Leu Asn	
390 395 400	
gtg aag ttg acc aag cta act gag aag caa gcc cag tac ctg ggc atg	1304
Val Lys Leu Thr Lys Leu Thr Glu Lys Gln Ala Gln Tyr Leu Gly Met	
405 410 415	
tcc tgt gat ggc ccc ttc aag ccg gat cac tac cgc tac tga	1346
Ser Cys Asp Gly Pro Phe Lys Pro Asp His Tyr Arg Tyr	
420 425 430	
gagccaggtc tgcgtttcac cctccagctg ctgtccttgc ccaggcccca cctctcctcc	1406
ctaagagcta atggcaccaa ctttgtgact ggttttgtcag tgtcccccat cgactctctg	1466
gggctgatca cttagtTTTTT ggctcttgct gcagccgtca tactgttcca aatgtggcag	1526
cgggaacaga gtaccctctt caagccccgg tcatgatgga ggtcccagcc acagggaacc	1586
atgagctcag tggctcttgga acagctcact aagtcagtc ttccttagcc tggaagccag	1646
tagtggagtc acaaagccca tgtgttttgc catctaggcc ttcacctgggt ctgtggactt	1706
atacctgtgt gcttggttta caggtccagt gggtcttcag cccatgacag atgagaagg	1766
gctatatattga agggcaaaga ggaactgttg tttgaatttt cctgagagcc tggcttagtg	1826
ctgggccttc tcttaaacct cattacaatg aggttagtac ttttagtccc tgttttacag	1886
gggttagaat agactgttaa ggggcaactg agaaagaaca gagaagtgac agctaggggt	1946
tgagaggggc cagaaaaaca tgaatgcagg cagatttcgt gaaatctgcc accactttat	2006
aaccagatgg ttcctttcac aaccctgggt caaaaagaga ataatttggc ctataatgtt	2066
aaaagaaagc aggaaggtgg gtaaataaaa atcttggtgc ctgg	2110

<210> 32
 <211> 432
 <212> PRT

<213> Homo sapiens

<400> 32

Met Ser Asp Lys Leu Pro Tyr Lys Val Ala Asp Ile Gly Leu Ala Ala
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Trp Gly Arg Lys Ala Leu Asp Ile Ala Glu Asn Glu Met Pro Gly Leu
20 25 30

Met Arg Met Arg Glu Arg Tyr Ser Ala Ser Lys Pro Leu Lys Gly Ala
35 40 45

Arg Ile Ala Gly Cys Leu His Met Thr Val Glu Thr Ala Val Leu Ile
50 55 60

Glu Thr Leu Val Thr Leu Gly Ala Glu Val Gln Trp Ser Ser Cys Asn
65 70 75 80

Ile Phe Ser Thr Gln Asp His Ala Ala Ala Ile Ala Lys Ala Gly
85 90 95

Ile Pro Val Tyr Ala Trp Lys Gly Glu Thr Asp Glu Glu Tyr Leu Trp
100 105 110

Cys Ile Glu Gln Thr Leu Tyr Phe Lys Asp Gly Pro Leu Asn Met Ile
115 120 125

Leu Asp Asp Gly Gly Asp Leu Thr Asn Leu Ile His Thr Lys Tyr Pro
130 135 140

Gln Leu Leu Pro Gly Ile Arg Gly Ile Ser Glu Glu Thr Thr Thr Gly
145 150 155 160

Val His Asn Leu Tyr Lys Met Met Ala Asn Gly Ile Leu Lys Val Pro
165 170 175

Ala Ile Asn Val Asn Asp Ser Val Thr Lys Ser Lys Phe Asp Asn Leu
180 185 190

91/201

Tyr Gly Cys Arg Glu Ser Leu Ile Asp Gly Ile Lys Arg Ala Thr Asp
195 200 205

Val Met Ile Ala Gly Lys Val Ala Val Val Ala Gly Tyr Gly Asp Val
210 215 220

Gly Lys Gly Cys Ala Gln Ala Leu Arg Gly Phe Gly Ala Arg Val Ile
225 230 235 240

Ile Thr Glu Ile Asp Pro Ile Asn Ala Leu Gln Ala Ala Met Glu Gly
245 250 255

Tyr Glu Val Thr Thr Met Asp Glu Ala Cys Gln Glu Gly Asn Ile Phe
260 265 270

Val Thr Thr Thr Gly Cys Ile Asp Ile Ile Leu Gly Arg His Phe Glu
275 280 285

Gln Met Lys Asp Asp Ala Ile Val Cys Asn Ile Gly His Phe Asp Val
290 295 300

Glu Ile Asp Val Lys Trp Leu Asn Glu Asn Ala Val Glu Lys Val Asn
305 310 315 320

Ile Lys Pro Gln Val Asp Arg Tyr Arg Leu Lys Asn Gly Arg Arg Ile
325 330 335

Ile Leu Leu Ala Glu Gly Arg Leu Val Asn Leu Gly Cys Ala Met Gly
340 345 350

His Pro Ser Phe Val Met Ser Asn Ser Phe Thr Asn Gln Val Met Ala
355 360 365

Gln Ile Glu Leu Trp Thr His Pro Asp Lys Tyr Pro Val Gly Val His
370 375 380

Phe Leu Pro Lys Lys Leu Asp Glu Ala Val Ala Glu Ala His Leu Gly
 385 390 395 400

Lys Leu Asn Val Lys Leu Thr Lys Leu Thr Glu Lys Gln Ala Gln Tyr
 405 410 415

Leu Gly Met Ser Cys Asp Gly Pro Phe Lys Pro Asp His Tyr Arg Tyr
 420 425 430

<210> 33
 <211> 1698
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (191).. (1309)
 <223>

<400> 33
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 ttctgcccgg caccgcgcct gccctctgcc gcgctccgcc ctgccgccga ccgcacgccc 180
 gccgcgggac atg gca cac gca ccg gca cgc tgc ccc agc gcc cgg ggc 229
 Met Ala His Ala Pro Ala Arg Cys Pro Ser Ala Arg Gly
 1 5 10
 tcc ggg gac ggc gag atg ggc aag ccc agg aac gtg gcg ctc atc acc 277
 Ser Gly Asp Gly Glu Met Gly Lys Pro Arg Asn Val Ala Leu Ile Thr
 15 20 25
 ggt atc aca ggc cag gat ggt tcc tac ctg gct gag ttc ctg ctg gag 325
 Gly Ile Thr Gly Gln Asp Gly Ser Tyr Leu Ala Glu Phe Leu Leu Glu
 30 35 40 45
 aaa ggc tat gag gtc cat gga att gta cgg cgg tcc agt tca ttt aat 373
 Lys Gly Tyr Glu Val His Gly Ile Val Arg Arg Ser Ser Ser Phe Asn
 50 55 60
 acg ggt cga att gag cat ctg tat aag aat ccc cag gct cac att gaa 421
 Thr Gly Arg Ile Glu His Leu Tyr Lys Asn Pro Gln Ala His Ile Glu
 65 70 75
 gga aac atg aag ttg cac tat ggc gat ctc act gac agt acc tgc ctt 469
 93/201

Gly	Asn	Met	Lys	Leu	His	Tyr	Gly	Asp	Leu	Thr	Asp	Ser	Thr	Cys	Leu	
	80						85					90				
gtg	aag	atc	att	aat	gaa	gta	aag	ccc	aca	gag	atc	tac	aac	ctt	gga	517
Val	Lys	Ile	Ile	Asn	Glu	Val	Lys	Pro	Thr	Glu	Ile	Tyr	Asn	Leu	Gly	
	95						100				105					
gcc	cag	agc	cac	gtc	aaa	att	tcc	ttt	gac	ctc	gct	gag	tac	act	gcg	565
Ala	Gln	Ser	His	Val	Lys	Ile	Ser	Phe	Asp	Leu	Ala	Glu	Tyr	Thr	Ala	
110					115					120					125	
gac	gtt	gac	gga	gtt	ggc	act	cta	cga	ctt	cta	gat	gca	gtt	aag	act	613
Asp	Val	Asp	Gly	Val	Gly	Thr	Leu	Arg	Leu	Leu	Asp	Ala	Val	Lys	Thr	
				130				135						140		
tgt	ggc	ctt	atc	aac	tct	gtg	aag	ttc	tac	caa	gcc	tca	aca	agt	gaa	661
Cys	Gly	Leu	Ile	Asn	Ser	Val	Lys	Phe	Tyr	Gln	Ala	Ser	Thr	Ser	Glu	
			145					150					155			
ctt	tat	ggg	aaa	gtg	cag	gaa	ata	ccc	cag	aag	gag	acc	acc	cct	ttc	709
Leu	Tyr	Gly	Lys	Val	Gln	Glu	Ile	Pro	Gln	Lys	Glu	Thr	Thr	Pro	Phe	
		160					165					170				
tat	ccc	cgg	tca	ccc	tat	ggg	gca	gca	aaa	ctc	tat	gcc	tat	tgg	att	757
Tyr	Pro	Arg	Ser	Pro	Tyr	Gly	Ala	Ala	Lys	Leu	Tyr	Ala	Tyr	Trp	Ile	
	175					180					185					
gtg	gtg	aac	ttc	cgt	gag	gcg	tat	aat	ctc	ttt	gca	gtg	aac	ggc	att	805
Val	Val	Asn	Phe	Arg	Glu	Ala	Tyr	Asn	Leu	Phe	Ala	Val	Asn	Gly	Ile	
190					195					200					205	
ctc	ttc	aat	cat	gag	agt	ccc	aga	aga	gga	gct	aat	ttc	gtt	act	cga	853
Leu	Phe	Asn	His	Glu	Ser	Pro	Arg	Arg	Gly	Ala	Asn	Phe	Val	Thr	Arg	
				210				215						220		
aaa	att	agc	cgg	tca	gta	gct	aag	att	tac	ctt	gga	caa	ctg	gaa	tgt	901
Lys	Ile	Ser	Arg	Ser	Val	Ala	Lys	Ile	Tyr	Leu	Gly	Gln	Leu	Glu	Cys	
			225					230					235			
ttc	agt	ttg	gga	aat	ctg	gat	gcc	aaa	cga	gat	tgg	ggc	cat	gcc	aag	949
Phe	Ser	Leu	Gly	Asn	Leu	Asp	Ala	Lys	Arg	Asp	Trp	Gly	His	Ala	Lys	
		240					245					250				
gac	tat	gtg	gag	gct	atg	tgg	ttg	atg	ttg	cag	aat	gat	gag	ccg	gag	997
Asp	Tyr	Val	Glu	Ala	Met	Trp	Leu	Met	Leu	Gln	Asn	Asp	Glu	Pro	Glu	
	255					260					265					
gac	ttc	gtt	ata	gct	act	ggg	gag	gtc	cat	agt	gtc	cgg	gaa	ttt	gtc	1045
Asp	Phe	Val	Ile	Ala	Thr	Gly	Glu	Val	His	Ser	Val	Arg	Glu	Phe	Val	
270					275					280					285	

gag	aaa	tca	ttc	ttg	cac	att	gga	aaa	acc	att	gtg	tgg	gaa	gga	aag	1093
Glu	Lys	Ser	Phe	Leu	His	Ile	Gly	Lys	Thr	Ile	Val	Trp	Glu	Gly	Lys	
				290					295						300	

aat	gaa	aat	gaa	gtg	ggc	aga	tgt	aaa	gag	acc	ggc	aaa	gtt	cac	gtg	1141
Asn	Glu	Asn	Glu	Val	Gly	Arg	Cys	Lys	Glu	Thr	Gly	Lys	Val	His	Val	
				305				310					315			

act	gtg	gat	ctc	aag	tac	tac	cgg	cca	act	gaa	gtg	gac	ttt	ctg	cag	1189
Thr	Val	Asp	Leu	Lys	Tyr	Tyr	Arg	Pro	Thr	Glu	Val	Asp	Phe	Leu	Gln	
				320			325					330				

ggc	gac	tgc	acc	aaa	gcg	aaa	cag	aag	ctg	aac	tgg	aag	ccc	cgg	gtc	1237
Gly	Asp	Cys	Thr	Lys	Ala	Lys	Gln	Lys	Leu	Asn	Trp	Lys	Pro	Arg	Val	
	335					340					345					

gct	ttc	gat	gag	ctg	gtg	agg	gag	atg	gtg	cac	gcc	gac	gtg	gag	ctc	1285
Ala	Phe	Asp	Glu	Leu	Val	Arg	Glu	Met	Val	His	Ala	Asp	Val	Glu	Leu	
350					355				360					365		

atg	agg	aca	aac	ccc	aat	gcc	tga	gcagcgcctc	ggagcccggc	ccgccctccg	1339
Met	Arg	Thr	Asn	Pro	Asn	Ala					
				370							

gctacaatcc	ccgcagagtc	tccggtgcag	acgcgctgcg	gggatgggga	gcggcgtgcc	1399
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aatctgcggg	tcccctgcgg	cccctgctgc	cgtgcgctg	tcccggccgc	aagagcgggg	1459
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ccgccccgcc	gaggtttgta	gcagccggga	tgtgaccctc	cagggtttgg	gtcgctttgc	1519
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gtttgtcgaa	gcctcctctg	aatggctttg	tgaaatcaag	atgttttaat	cacattcact	1579
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ttacttgaaa	ttatgttggt	acacaacaaa	ttgtggggcc	ttcaaattgt	ttttctcttt	1639
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	20		25		30														
Gly	Gln	Asp	Gly	Ser	Tyr	Leu	Ala	Glu	Phe	Leu	Leu	Glu	Lys	Gly	Tyr				
	35						40					45							
Glu	Val	His	Gly	Ile	Val	Arg	Arg	Ser	Ser	Ser	Phe	Asn	Thr	Gly	Arg				
	50					55					60								
Ile	Glu	His	Leu	Tyr	Lys	Asn	Pro	Gln	Ala	His	Ile	Glu	Gly	Asn	Met				
65					70					75					80				
Lys	Leu	His	Tyr	Gly	Asp	Leu	Thr	Asp	Ser	Thr	Cys	Leu	Val	Lys	Ile				
				85					90					95					
Ile	Asn	Glu	Val	Lys	Pro	Thr	Glu	Ile	Tyr	Asn	Leu	Gly	Ala	Gln	Ser				
			100					105					110						
His	Val	Lys	Ile	Ser	Phe	Asp	Leu	Ala	Glu	Tyr	Thr	Ala	Asp	Val	Asp				
		115					120					125							
Gly	Val	Gly	Thr	Leu	Arg	Leu	Leu	Asp	Ala	Val	Lys	Thr	Cys	Gly	Leu				
	130					135					140								
Ile	Asn	Ser	Val	Lys	Phe	Tyr	Gln	Ala	Ser	Thr	Ser	Glu	Leu	Tyr	Gly				
145					150					155					160				
Lys	Val	Gln	Glu	Ile	Pro	Gln	Lys	Glu	Thr	Thr	Pro	Phe	Tyr	Pro	Arg				
				165					170					175					
Ser	Pro	Tyr	Gly	Ala	Ala	Lys	Leu	Tyr	Ala	Tyr	Trp	Ile	Val	Val	Asn				
			180					185					190						
Phe	Arg	Glu	Ala	Tyr	Asn	Leu	Phe	Ala	Val	Asn	Gly	Ile	Leu	Phe	Asn				
		195					200					205							
His	Glu	Ser	Pro	Arg	Arg	Gly	Ala	Asn	Phe	Val	Thr	Arg	Lys	Ile	Ser				
	210					215					220								

Arg Ser Val Ala Lys Ile Tyr Leu Gly Gln Leu Glu Cys Phe Ser Leu
225 230 235 240

Gly Asn Leu Asp Ala Lys Arg Asp Trp Gly His Ala Lys Asp Tyr Val
245 250 255

Glu Ala Met Trp Leu Met Leu Gln Asn Asp Glu Pro Glu Asp Phe Val
260 265 270

Ile Ala Thr Gly Glu Val His Ser Val Arg Glu Phe Val Glu Lys Ser
275 280 285

Phe Leu His Ile Gly Lys Thr Ile Val Trp Glu Gly Lys Asn Glu Asn
290 295 300

Glu Val Gly Arg Cys Lys Glu Thr Gly Lys Val His Val Thr Val Asp
305 310 315 320

Leu Lys Tyr Tyr Arg Pro Thr Glu Val Asp Phe Leu Gln Gly Asp Cys
325 330 335

Thr Lys Ala Lys Gln Lys Leu Asn Trp Lys Pro Arg Val Ala Phe Asp
340 345 350

Glu Leu Val Arg Glu Met Val His Ala Asp Val Glu Leu Met Arg Thr
355 360 365

Asn Pro Asn Ala
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Leu Ser Arg Phe Ser Ala Phe Arg Ile Leu Arg Ser Arg Gly Tyr Ile	
10 15 20 25	
tgc cgc aat ttt aca ggg tct tct gct ttg ctg acc aga acc cat att	148
Cys Arg Asn Phe Thr Gly Ser Ser Ala Leu Leu Thr Arg Thr His Ile	
30 35 40	
aac tat gga gtc aaa ggg gat gtg gca gtt gtt cga att aac tct ccc	196
Asn Tyr Gly Val Lys Gly Asp Val Ala Val Val Arg Ile Asn Ser Pro	
45 50 55	
aat tca aag gta aat aca ctg agt aaa gag cta cat tca gag ttc tca	244
Asn Ser Lys Val Asn Thr Leu Ser Lys Glu Leu His Ser Glu Phe Ser	
60 65 70	
gaa gtt atg aat gaa atc tgg gct agt gat caa atc aga agt gcc gtc	292
Glu Val Met Asn Glu Ile Trp Ala Ser Asp Gln Ile Arg Ser Ala Val	
75 80 85	
ctt atc tca tca aag cca ggc tgc ttt att gca ggt gct gat atc aac	340
Leu Ile Ser Ser Lys Pro Gly Cys Phe Ile Ala Gly Ala Asp Ile Asn	
90 95 100 105	
atg tta gcc gct tgc aag acc ctt caa gaa gta aca cag cta tca caa	388
Met Leu Ala Ala Cys Lys Thr Leu Gln Glu Val Thr Gln Leu Ser Gln	
110 115 120	
gaa gca cag aga ata gtt gag aaa ctt gaa aag tcc aca aag cct att	436
Glu Ala Gln Arg Ile Val Glu Lys Leu Glu Lys Ser Thr Lys Pro Ile	
125 130 135	
gtg gct gcc atc aat gga tcc tgc ctg gga gga gga ctt gag gtt gcc	484
Val Ala Ala Ile Asn Gly Ser Cys Leu Gly Gly Gly Leu Glu Val Ala	
140 145 150	
att tca tgc caa tac aga ata gca aca aaa gac aga aaa aca gta tta	532
Ile Ser Cys Gln Tyr Arg Ile Ala Thr Lys Asp Arg Lys Thr Val Leu	
155 160 165	
ggt acc cct gaa gtt ttg ctg ggg gcc tta cca gga gca gga ggc aca	580
Gly Thr Pro Glu Val Leu Leu Gly Ala Leu Pro Gly Ala Gly Gly Thr	
170 175 180 185	

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190 195 200	
ctg act ggt aga agc att cgt gca gac agg gca aag aaa atg gga ctg Leu Thr Gly Arg Ser Ile Arg Ala Asp Arg Ala Lys Lys Met Gly Leu	676
205 210 215	
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220 225 230	
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235 240 245	
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250 255 260 265	
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270 275 280	
gtt tac aaa aaa gtg gaa gaa aaa gtg cga aag cag act aaa ggc ctt Val Tyr Lys Lys Val Glu Glu Lys Val Arg Lys Gln Thr Lys Gly Leu	916
285 290 295	
tat cct gca cct ctg aaa ata att gat gtg gta aag act gga att gag Tyr Pro Ala Pro Leu Lys Ile Ile Asp Val Val Lys Thr Gly Ile Glu	964
300 305 310	
caa ggg agt gat gcc ggt tat ctc tgt gaa tct cag aaa ttt gga gag Gln Gly Ser Asp Ala Gly Tyr Leu Cys Glu Ser Gln Lys Phe Gly Glu	1012
315 320 325	
ctt gta atg acc aaa gaa tca aag gcc ttg atg gga ctc tac cat ggt Leu Val Met Thr Lys Glu Ser Lys Ala Leu Met Gly Leu Tyr His Gly	1060
330 335 340 345	
cag gtc ctg tgc aag aag aat aaa ttt gga gct cca cag aag gat gtt Gln Val Leu Cys Lys Lys Asn Lys Phe Gly Ala Pro Gln Lys Asp Val	1108
350 355 360	
aag cat ctg gct att ctt ggt gca ggg ctg atg gga gca ggc atc gcc Lys His Leu Ala Ile Leu Gly Ala Gly Leu Met Gly Ala Gly Ile Ala	1156
365 370 375	
caa gtc tcc gtg gat aag ggg cta aag act ata ctt aaa gat gcc acc Gln Val Ser Val Asp Lys Gly Leu Lys Thr Ile Leu Lys Asp Ala Thr	1204

380	385	390	
ctc act gcg cta gac cga gga cag caa caa gtg ttc aaa gga ttg aat Leu Thr Ala Leu Asp Arg Gly Gln Gln Gln Val Phe Lys Gly Leu Asn 395 400 405			1252
gac aaa gtg aag aag aaa gct cta aca tca ttt gaa agg gat tcc atc Asp Lys Val Lys Lys Lys Ala Leu Thr Ser Phe Glu Arg Asp Ser Ile 410 415 420 425			1300
ttc agc aac ttg act ggg cag ctt gat tac caa ggt ttt gaa aag gcc Phe Ser Asn Leu Thr Gly Gln Leu Asp Tyr Gln Gly Phe Glu Lys Ala 430 435 440			1348
gac atg gtg att gaa gct gtg ttt gag gac ctt agt ctt aag cac aga Asp Met Val Ile Glu Ala Val Phe Glu Asp Leu Ser Leu Lys His Arg 445 450 455			1396
gtg cta aag gaa gta gaa gcg gtg att cca gat cac tgt atc ttt gcc Val Leu Lys Glu Val Glu Ala Val Ile Pro Asp His Cys Ile Phe Ala 460 465 470			1444
agt aac aca tct gct ctc cca atc agt gaa atc gct gct gtc agc aaa Ser Asn Thr Ser Ala Leu Pro Ile Ser Glu Ile Ala Ala Val Ser Lys 475 480 485			1492
aga cct gag aag gtg att ggc atg cac tac ttc tct ccc gtg gac aag Arg Pro Glu Lys Val Ile Gly Met His Tyr Phe Ser Pro Val Asp Lys 490 495 500 505			1540
atg cag ctg ctg gag att atc acg acc gag aaa act tcc aaa gac acc Met Gln Leu Leu Glu Ile Ile Thr Thr Glu Lys Thr Ser Lys Asp Thr 510 515 520			1588
agt gct tca gct gta gca gtt ggt ctc aag cag ggg aag gtc atc att Ser Ala Ser Ala Val Ala Val Gly Leu Lys Gln Gly Lys Val Ile Ile 525 530 535			1636
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atg atg tct gaa gtc atc cga atc ctc cag gaa gga gtt gac ccg aag Met Met Ser Glu Val Ile Arg Ile Leu Gln Glu Gly Val Asp Pro Lys 555 560 565			1732
aag ctg gat tcc ctg acc aca agc ttt ggc ttt cct gtg ggt gcc gcc Lys Leu Asp Ser Leu Thr Thr Ser Phe Gly Phe Pro Val Gly Ala Ala 570 575 580 585			1780

aca ctg gtg gat gaa gtt ggt gtg gat gta gcg aaa cat gtg gcg gaa Thr Leu Val Asp Glu Val Gly Val Asp Val Ala Lys His Val Ala Glu 590 595 600	1828
gat ctg ggc aaa gtc ttt ggg gag cgg ttt gga ggt gga aac cca gaa Asp Leu Gly Lys Val Phe Gly Glu Arg Phe Gly Gly Gly Asn Pro Glu 605 610 615	1876
ctg ctg aca cag atg gtg tcc aag ggc ttc cta ggt cgt aaa tct ggg Leu Leu Thr Gln Met Val Ser Lys Gly Phe Leu Gly Arg Lys Ser Gly 620 625 630	1924
aag ggc ttt tac atc tat cag gag ggt gtg aag agg aag gat ttg aat Lys Gly Phe Tyr Ile Tyr Gln Glu Gly Val Lys Arg Lys Asp Leu Asn 635 640 645	1972
tct gac atg gat agt att tta gcg agt ctg aag ctg cct cct aag tct Ser Asp Met Asp Ser Ile Leu Ala Ser Leu Lys Leu Pro Pro Lys Ser 650 655 660 665	2020
gaa gtc tca tca gac gaa gac atc cag ttc cgc ctg gtg aca aga ttt Glu Val Ser Ser Asp Glu Asp Ile Gln Phe Arg Leu Val Thr Arg Phe 670 675 680	2068
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gca gag gga gac atc gga gcc gtc ttt ggg ctt ggc ttc ccg cct tgt Ala Glu Gly Asp Ile Gly Ala Val Phe Gly Leu Gly Phe Pro Pro Cys 700 705 710	2164
ctg gga ggg cct ttc cgc ttt gtg gat ctg tat ggc gcc cag aag ata Leu Gly Gly Pro Phe Arg Phe Val Asp Leu Tyr Gly Ala Gln Lys Ile 715 720 725	2212
gtg gac cgg ctc aag aaa tat gaa gct gcc tat gga aaa cag ttc acc Val Asp Arg Leu Lys Lys Tyr Glu Ala Ala Tyr Gly Lys Gln Phe Thr 730 735 740 745	2260
cca tgc cag ctg cta gct gac cat gct aac agc cct aac aag aag ttc Pro Cys Gln Leu Leu Ala Asp His Ala Asn Ser Pro Asn Lys Lys Phe 750 755 760	2308
tac cag tga gcaggcctca tgccctcgctc agtcagtgca ctaaccccag Tyr Gln	2357
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 aaaaaa 2963

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<400> 36

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Ser Ala Leu Leu Thr Arg Thr His Ile Asn Tyr Gly Val Lys Gly Asp
 35 40 45

Val Ala Val Val Arg Ile Asn Ser Pro Asn Ser Lys Val Asn Thr Leu
 50 55 60

Ser Lys Glu Leu His Ser Glu Phe Ser Glu Val Met Asn Glu Ile Trp
 65 70 75 80

Ala Ser Asp Gln Ile Arg Ser Ala Val Leu Ile Ser Ser Lys Pro Gly
 85 90 95

Cys Phe Ile Ala Gly Ala Asp Ile Asn Met Leu Ala Ala Cys Lys Thr
100 105 110

Leu Gln Glu Val Thr Gln Leu Ser Gln Glu Ala Gln Arg Ile Val Glu
115 120 125

Lys Leu Glu Lys Ser Thr Lys Pro Ile Val Ala Ala Ile Asn Gly Ser
130 135 140

Cys Leu Gly Gly Gly Leu Glu Val Ala Ile Ser Cys Gln Tyr Arg Ile
145 150 155 160

Ala Thr Lys Asp Arg Lys Thr Val Leu Gly Thr Pro Glu Val Leu Leu
165 170 175

Gly Ala Leu Pro Gly Ala Gly Gly Thr Gln Arg Leu Pro Lys Met Val
180 185 190

Gly Val Pro Ala Ala Leu Asp Met Met Leu Thr Gly Arg Ser Ile Arg
195 200 205

Ala Asp Arg Ala Lys Lys Met Gly Leu Val Asp Gln Leu Val Glu Pro
210 215 220

Leu Gly Pro Gly Leu Lys Pro Pro Glu Glu Arg Thr Ile Glu Tyr Leu
225 230 235 240

Glu Glu Val Ala Ile Thr Phe Ala Lys Gly Leu Ala Asp Lys Lys Ile
245 250 255

Ser Pro Lys Arg Asp Lys Gly Leu Val Glu Lys Leu Thr Ala Tyr Ala
260 265 270

Met Thr Ile Pro Phe Val Arg Gln Gln Val Tyr Lys Lys Val Glu Glu
275 280 285

Lys Val Arg Lys Gln Thr Lys Gly Leu Tyr Pro Ala Pro Leu Lys Ile
290 295 300

Ile Asp Val Val Lys Thr Gly Ile Glu Gln Gly Ser Asp Ala Gly Tyr
305 310 315 320

Leu Cys Glu Ser Gln Lys Phe Gly Glu Leu Val Met Thr Lys Glu Ser
325 330 335

Lys Ala Leu Met Gly Leu Tyr His Gly Gln Val Leu Cys Lys Lys Asn
340 345 350

Lys Phe Gly Ala Pro Gln Lys Asp Val Lys His Leu Ala Ile Leu Gly
355 360 365

Ala Gly Leu Met Gly Ala Gly Ile Ala Gln Val Ser Val Asp Lys Gly
370 375 380

Leu Lys Thr Ile Leu Lys Asp Ala Thr Leu Thr Ala Leu Asp Arg Gly
385 390 395 400

Gln Gln Gln Val Phe Lys Gly Leu Asn Asp Lys Val Lys Lys Lys Ala
405 410 415

Leu Thr Ser Phe Glu Arg Asp Ser Ile Phe Ser Asn Leu Thr Gly Gln
420 425 430

Leu Asp Tyr Gln Gly Phe Glu Lys Ala Asp Met Val Ile Glu Ala Val
435 440 445

Phe Glu Asp Leu Ser Leu Lys His Arg Val Leu Lys Glu Val Glu Ala
450 455 460

Val Ile Pro Asp His Cys Ile Phe Ala Ser Asn Thr Ser Ala Leu Pro
465 470 475 480

Ile Ser Glu Ile Ala Ala Val Ser Lys Arg Pro Glu Lys Val Ile Gly
485 490 495

Met His Tyr Phe Ser Pro Val Asp Lys Met Gln Leu Leu Glu Ile Ile
500 505 510

Thr Thr Glu Lys Thr Ser Lys Asp Thr Ser Ala Ser Ala Val Ala Val
515 520 525

Gly Leu Lys Gln Gly Lys Val Ile Ile Val Val Lys Asp Gly Pro Gly
530 535 540

Phe Tyr Thr Thr Arg Cys Leu Ala Pro Met Met Ser Glu Val Ile Arg
545 550 555 560

Ile Leu Gln Glu Gly Val Asp Pro Lys Lys Leu Asp Ser Leu Thr Thr
565 570 575

Ser Phe Gly Phe Pro Val Gly Ala Ala Thr Leu Val Asp Glu Val Gly
580 585 590

Val Asp Val Ala Lys His Val Ala Glu Asp Leu Gly Lys Val Phe Gly
595 600 605

Glu Arg Phe Gly Gly Gly Asn Pro Glu Leu Leu Thr Gln Met Val Ser
610 615 620

Lys Gly Phe Leu Gly Arg Lys Ser Gly Lys Gly Phe Tyr Ile Tyr Gln
625 630 635 640

Glu Gly Val Lys Arg Lys Asp Leu Asn Ser Asp Met Asp Ser Ile Leu
645 650 655

Ala Ser Leu Lys Leu Pro Pro Lys Ser Glu Val Ser Ser Asp Glu Asp
660 665 670

Ile Gln Phe Arg Leu Val Thr Arg Phe Val Asn Glu Ala Val Met Cys
675 680 685

Leu Gln Glu Gly Ile Leu Ala Thr Pro Ala Glu Gly Asp Ile Gly Ala
690 695 700

Val Phe Gly Leu Gly Phe Pro Pro Cys Leu Gly Gly Pro Phe Arg Phe
705 710 715 720

Val Asp Leu Tyr Gly Ala Gln Lys Ile Val Asp Arg Leu Lys Lys Tyr
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Ala Leu Leu Cys Leu Ala Val Ala Ala Leu Val Arg Ala Asp Ala Pro
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Glu Glu Glu Asp His Val Leu Val Leu Arg Lys Ser Asn Phe Ala Glu
25 30 35

gcg ctg gcg gcc cac aag tac ctg ctg gtg gag ttc tat gcc cct tgg 200
Ala Leu Ala Ala His Lys Tyr Leu Leu Val Glu Phe Tyr Ala Pro Trp
40 45 50

tgt ggc cac tgc aag gct ctg gcc cct gag tat gcc aaa gcc gct ggg 248
Cys Gly His Cys Lys Ala Leu Ala Pro Glu Tyr Ala Lys Ala Ala Gly
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acg gag gag tct gac ctg gcc cag cag tac ggc gtg cgc ggc tat ccc Thr Glu Glu Ser Asp Leu Ala Gln Gln Tyr Gly Val Arg Gly Tyr Pro 85 90 95 100	344
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ttg gtg gag tcc agc gag gtg gct gtc atc ggc ttc ttc aag gac gtg Leu Val Glu Ser Ser Glu Val Ala Val Ile Gly Phe Phe Lys Asp Val 150 155 160	536
gag tcg gac tct gcc aag cag ttt ttg cag gca gca gag gcc atc gat Glu Ser Asp Ser Ala Lys Gln Phe Leu Gln Ala Ala Glu Ala Ile Asp 165 170 175 180	584
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cag ctc gac aaa gat ggg gtt gtc ctc ttt aag aag ttt gat gaa ggc Gln Leu Asp Lys Asp Gly Val Val Leu Phe Lys Lys Phe Asp Glu Gly 200 205 210	680
cgg aac aac ttt gaa ggg gag gtc acc aag gag aac ctg ctg gac ttt Arg Asn Asn Phe Glu Gly Glu Val Thr Lys Glu Asn Leu Leu Asp Phe 215 220 225	728
atc aaa cac aac cag ctg ccc ctt gtc atc gag ttc acc gag cag aca Ile Lys His Asn Gln Leu Pro Leu Val Ile Glu Phe Thr Glu Gln Thr 230 235 240	776
gcc ccg aag att ttt gga ggt gaa atc aag act cac atc ctg ctg ttc Ala Pro Lys Ile Phe Gly Gly Glu Ile Lys Thr His Ile Leu Leu Phe 245 250 255 260	824
ttg ccc aag agt gtg tct gac tat gac ggc aaa ctg agc aac ttc aaa 107/201	872

Leu	Pro	Lys	Ser	Val	Ser	Asp	Tyr	Asp	Gly	Lys	Leu	Ser	Asn	Phe	Lys	
				265					270					275		
aca	gca	gcc	gag	agc	ttc	aag	ggc	aag	atc	ctg	ttc	atc	ttc	atc	gac	920
Thr	Ala	Ala	Glu	Ser	Phe	Lys	Gly	Lys	Ile	Leu	Phe	Ile	Phe	Ile	Asp	
			280					285					290			
agc	gac	cac	acc	gac	aac	cag	cgc	atc	ctc	gag	ttc	ttt	ggc	ctg	aag	968
Ser	Asp	His	Thr	Asp	Asn	Gln	Arg	Ile	Leu	Glu	Phe	Phe	Gly	Leu	Lys	
		295					300					305				
aag	gaa	gag	tgc	ccg	gcc	gtg	cgc	ctc	atc	acc	ctg	gag	gag	gag	atg	1016
Lys	Glu	Glu	Cys	Pro	Ala	Val	Arg	Leu	Ile	Thr	Leu	Glu	Glu	Glu	Met	
	310					315					320					
acc	aag	tac	aag	ccc	gaa	tcg	gag	gag	ctg	acg	gca	gag	agg	atc	aca	1064
Thr	Lys	Tyr	Lys	Pro	Glu	Ser	Glu	Glu	Leu	Thr	Ala	Glu	Arg	Ile	Thr	
325					330					335					340	
gag	ttc	tgc	cac	cgc	ttc	ctg	gag	ggc	aaa	atc	aag	ccc	cac	ctg	atg	1112
Glu	Phe	Cys	His	Arg	Phe	Leu	Glu	Gly	Lys	Ile	Lys	Pro	His	Leu	Met	
				345					350					355		
agc	cag	gag	ctg	ccg	gag	gac	tgg	gac	aag	cag	cct	gtc	aag	gtg	ctt	1160
Ser	Gln	Glu	Leu	Pro	Glu	Asp	Trp	Asp	Lys	Gln	Pro	Val	Lys	Val	Leu	
			360					365					370			
gtt	ggg	aag	aac	ttt	gaa	gac	gtg	gct	ttt	gat	gag	aaa	aaa	aac	gtc	1208
Val	Gly	Lys	Asn	Phe	Glu	Asp	Val	Ala	Phe	Asp	Glu	Lys	Lys	Asn	Val	
		375					380					385				
ttt	gtg	gag	ttc	tat	gcc	cca	tgg	tgt	ggt	cac	tgc	aaa	cag	ttg	gct	1256
Phe	Val	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Gln	Leu	Ala	
	390					395					400					
ccc	att	tgg	gat	aaa	ctg	gga	gag	acg	tac	aag	gac	cat	gag	aac	atc	1304
Pro	Ile	Trp	Asp	Lys	Leu	Gly	Glu	Thr	Tyr	Lys	Asp	His	Glu	Asn	Ile	
405					410					415					420	
gtc	atc	gcc	aag	atg	gac	tcg	act	gcc	aac	gag	gtg	gag	gcc	gtc	aaa	1352
Val	Ile	Ala	Lys	Met	Asp	Ser	Thr	Ala	Asn	Glu	Val	Glu	Ala	Val	Lys	
				425					430					435		
gtg	cac	agc	ttc	ccc	aca	ctc	aag	ttc	ttt	cct	gcc	agt	gcc	gac	agg	1400
Val	His	Ser	Phe	Pro	Thr	Leu	Lys	Phe	Phe	Pro	Ala	Ser	Ala	Asp	Arg	
			440					445					450			
acg	gtc	att	gat	tac	aac	ggg	gaa	cgc	acg	ctg	gat	ggt	ttt	aag	aaa	1448
Thr	Val	Ile	Asp	Tyr	Asn	Gly	Glu	Arg	Thr	Leu	Asp	Gly	Phe	Lys	Lys	
		455					460					465				

ttc ctg gag agc ggt ggc cag gat ggg gca ggg gat gat gac gat ctc	1496
Phe Leu Glu Ser Gly Gly Gln Asp Gly Ala Gly Asp Asp Asp Asp Leu	
470 475 480	
gag gac ctg gaa gaa gca gag gag cca gac atg gag gaa gac gat gat	1544
Glu Asp Leu Glu Glu Ala Glu Glu Pro Asp Met Glu Glu Asp Asp Asp	
485 490 495 500	
cag aaa gct gtg aaa gat gaa ctg taa tacgcaaagc cagacccggg	1591
Gln Lys Ala Val Lys Asp Glu Leu	
505	
cgctgccgag acccctcggg ggctgcacac ccagcagcag cgcacgcctc cgaagcctgc	1651
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accctacac accgtccgtt ccccccgtc tcttccttct gcttttcggt ttttggaag	1771
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cccgcgggag gtttctctc tttttgaaaa ttccgtctgt gggattttta gacatttttc	1951
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tgatcatggc tcttgcatth ttgggtaa at ggagacttcc ggatcctgtc aggggtgtccc	2131
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aaaaaaa	2438

<210> 38
 <211> 508
 <212> PRT
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<400> 38

Met Leu Arg Arg Ala Leu Leu Cys Leu Ala Val Ala Ala Leu Val Arg
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20 25 30

Asn Phe Ala Glu Ala Leu Ala Ala His Lys Tyr Leu Leu Val Glu Phe
35 40 45

Tyr Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro Glu Tyr Ala
50 55 60

Lys Ala Ala Gly Lys Leu Lys Ala Glu Gly Ser Glu Ile Arg Leu Ala
65 70 75 80

Lys Val Asp Ala Thr Glu Glu Ser Asp Leu Ala Gln Gln Tyr Gly Val
85 90 95

Arg Gly Tyr Pro Thr Ile Lys Phe Phe Arg Asn Gly Asp Thr Ala Ser
100 105 110

Pro Lys Glu Tyr Thr Ala Gly Arg Glu Ala Asp Asp Ile Val Asn Trp
115 120 125

Leu Lys Lys Arg Thr Gly Pro Ala Ala Thr Thr Leu Pro Asp Gly Ala
130 135 140

Ala Ala Glu Ser Leu Val Glu Ser Ser Glu Val Ala Val Ile Gly Phe
145 150 155 160

Phe Lys Asp Val Glu Ser Asp Ser Ala Lys Gln Phe Leu Gln Ala Ala
165 170 175

Glu Ala Ile Asp Asp Ile Pro Phe Gly Ile Thr Ser Asn Ser Asp Val
180 185 190

Phe Ser Lys Tyr Gln Leu Asp Lys Asp Gly Val Val Leu Phe Lys Lys
110/201

195					200					205					
Phe	Asp	Glu	Gly	Arg	Asn	Asn	Phe	Glu	Gly	Glu	Val	Thr	Lys	Glu	Asn
210					215					220					
Leu	Leu	Asp	Phe	Ile	Lys	His	Asn	Gln	Leu	Pro	Leu	Val	Ile	Glu	Phe
225					230					235					240
Thr	Glu	Gln	Thr	Ala	Pro	Lys	Ile	Phe	Gly	Gly	Glu	Ile	Lys	Thr	His
				245					250					255	
Ile	Leu	Leu	Phe	Leu	Pro	Lys	Ser	Val	Ser	Asp	Tyr	Asp	Gly	Lys	Leu
			260					265					270		
Ser	Asn	Phe	Lys	Thr	Ala	Ala	Glu	Ser	Phe	Lys	Gly	Lys	Ile	Leu	Phe
		275					280					285			
Ile	Phe	Ile	Asp	Ser	Asp	His	Thr	Asp	Asn	Gln	Arg	Ile	Leu	Glu	Phe
	290					295					300				
Phe	Gly	Leu	Lys	Lys	Glu	Glu	Cys	Pro	Ala	Val	Arg	Leu	Ile	Thr	Leu
305					310					315					320
Glu	Glu	Glu	Met	Thr	Lys	Tyr	Lys	Pro	Glu	Ser	Glu	Glu	Leu	Thr	Ala
			325						330					335	
Glu	Arg	Ile	Thr	Glu	Phe	Cys	His	Arg	Phe	Leu	Glu	Gly	Lys	Ile	Lys
			340					345					350		
Pro	His	Leu	Met	Ser	Gln	Glu	Leu	Pro	Glu	Asp	Trp	Asp	Lys	Gln	Pro
		355					360					365			
Val	Lys	Val	Leu	Val	Gly	Lys	Asn	Phe	Glu	Asp	Val	Ala	Phe	Asp	Glu
	370					375					380				
Lys	Lys	Asn	Val	Phe	Val	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys
385					390					395					400

Lys Gln Leu Ala Pro Ile Trp Asp Lys Leu Gly Glu Thr Tyr Lys Asp
405 410 415

His Glu Asn Ile Val Ile Ala Lys Met Asp Ser Thr Ala Asn Glu Val
420 425 430

Glu Ala Val Lys Val His Ser Phe Pro Thr Leu Lys Phe Phe Pro Ala
435 440 445

Ser Ala Asp Arg Thr Val Ile Asp Tyr Asn Gly Glu Arg Thr Leu Asp
450 455 460

Gly Phe Lys Lys Phe Leu Glu Ser Gly Gly Gln Asp Gly Ala Gly Asp
465 470 475 480

Asp Asp Asp Leu Glu Asp Leu Glu Glu Ala Glu Glu Pro Asp Met Glu
485 490 495

Glu Asp Asp Asp Gln Lys Ala Val Lys Asp Glu Leu
500 505

<210> 39
<211> 959
<212> DNA
<213> Homo sapiens

<220>
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<222> (120).. (764)
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ccccgcctgc tgcggtggca ccagccagga ggcggagtgg aagtggccgt ggggcgggt 119

atg gga cta gct ggc gtg tgc gcc ctg aga cgc tca gcg ggc tat ata 167
Met Gly Leu Ala Gly Val Cys Ala Leu Arg Arg Ser Ala Gly Tyr Ile
1 5 10 15

ctc gtc ggt ggg gcc ggc ggt cag tct gcg gca gcg gca gca aga cgg 215
Leu Val Gly Gly Ala Gly Gly Gln Ser Ala Ala Ala Ala Arg Arg

20					25					30						
tgc	agt	gaa	gga	gag	tgg	gcg	tct	ggc	ggg	gtc	cgc	agt	ttc	agc	aga	263
Cys	Ser	Glu	Gly	Glu	Trp	Ala	Ser	Gly	Gly	Val	Arg	Ser	Phe	Ser	Arg	
		35					40					45				
gcc	gct	gca	gcc	atg	gcc	cca	atc	aag	gtg	gga	gat	gcc	atc	cca	gca	311
Ala	Ala	Ala	Ala	Met	Ala	Pro	Ile	Lys	Val	Gly	Asp	Ala	Ile	Pro	Ala	
		50				55					60					
gtg	gag	gtg	ttt	gaa	ggg	gag	cca	ggg	aac	aag	gtg	aac	ctg	gca	gag	359
Val	Glu	Val	Phe	Glu	Gly	Glu	Pro	Gly	Asn	Lys	Val	Asn	Leu	Ala	Glu	
65					70					75					80	
ctg	ttc	aag	ggc	aag	aag	ggt	gtg	ctg	ttt	gga	gtt	cct	ggg	gcc	ttc	407
Leu	Phe	Lys	Gly	Lys	Lys	Gly	Val	Leu	Phe	Gly	Val	Pro	Gly	Ala	Phe	
				85				90						95		
acc	cct	gga	tgt	tcc	aag	aca	cac	ctg	cca	ggg	ttt	gtg	gag	cag	gct	455
Thr	Pro	Gly	Cys	Ser	Lys	Thr	His	Leu	Pro	Gly	Phe	Val	Glu	Gln	Ala	
			100					105					110			
gag	gct	ctg	aag	gcc	aag	gga	gtc	cag	gtg	gtg	gcc	tgt	ctg	agt	gtt	503
Glu	Ala	Leu	Lys	Ala	Lys	Gly	Val	Gln	Val	Val	Ala	Cys	Leu	Ser	Val	
		115					120					125				
aat	gat	gcc	ttt	gtg	act	ggc	gag	tgg	ggc	cga	gcc	cac	aag	gcg	gaa	551
Asn	Asp	Ala	Phe	Val	Thr	Gly	Glu	Trp	Gly	Arg	Ala	His	Lys	Ala	Glu	
		130				135					140					
ggc	aag	gtt	cgg	ctc	ctg	gct	gat	ccc	act	ggg	gcc	ttt	ggg	aag	gag	599
Gly	Lys	Val	Arg	Leu	Leu	Ala	Asp	Pro	Thr	Gly	Ala	Phe	Gly	Lys	Glu	
145					150					155					160	
aca	gac	tta	tta	cta	gat	gat	tcg	ctg	gtg	tcc	atc	ttt	ggg	aat	cga	647
Thr	Asp	Leu	Leu	Leu	Asp	Asp	Ser	Leu	Val	Ser	Ile	Phe	Gly	Asn	Arg	
				165				170						175		
cgt	ctc	aag	agg	ttc	tcc	atg	gtg	gta	cag	gat	ggc	ata	gtg	aag	gcc	695
Arg	Leu	Lys	Arg	Phe	Ser	Met	Val	Val	Gln	Asp	Gly	Ile	Val	Lys	Ala	
			180					185					190			
ctg	aat	gtg	gaa	cca	gat	ggc	aca	ggc	ctc	acc	tgc	agc	ctg	gca	ccc	743
Leu	Asn	Val	Glu	Pro	Asp	Gly	Thr	Gly	Leu	Thr	Cys	Ser	Leu	Ala	Pro	
		195					200					205				
aat	atc	atc	tca	cag	ctc	tga	ggccctgggc	cagattactt	cctccacccc							794
Asn	Ile	Ile	Ser	Gln	Leu											
		210														

tccctatctc acctgcccag ccctgtgctg gggccctgca attggaatgt tggccagatt	854
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa	959

<210> 40
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 40

Met	Gly	Leu	Ala	Gly	Val	Cys	Ala	Leu	Arg	Arg	Ser	Ala	Gly	Tyr	Ile
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Leu	Val	Gly	Gly	Ala	Gly	Gly	Gln	Ser	Ala	Ala	Ala	Ala	Ala	Arg	Arg
		20						25						30	

Cys	Ser	Glu	Gly	Glu	Trp	Ala	Ser	Gly	Gly	Val	Arg	Ser	Phe	Ser	Arg
		35					40					45			

Ala	Ala	Ala	Ala	Met	Ala	Pro	Ile	Lys	Val	Gly	Asp	Ala	Ile	Pro	Ala
	50					55					60				

Val	Glu	Val	Phe	Glu	Gly	Glu	Pro	Gly	Asn	Lys	Val	Asn	Leu	Ala	Glu
65					70					75					80

Leu	Phe	Lys	Gly	Lys	Lys	Gly	Val	Leu	Phe	Gly	Val	Pro	Gly	Ala	Phe
				85					90					95	

Thr	Pro	Gly	Cys	Ser	Lys	Thr	His	Leu	Pro	Gly	Phe	Val	Glu	Gln	Ala
			100					105					110		

Glu	Ala	Leu	Lys	Ala	Lys	Gly	Val	Gln	Val	Val	Ala	Cys	Leu	Ser	Val
		115					120					125			

Asn	Asp	Ala	Phe	Val	Thr	Gly	Glu	Trp	Gly	Arg	Ala	His	Lys	Ala	Glu
	130						135				140				

Gly Lys Val Arg Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu
 145 150 155 160

Thr Asp Leu Leu Leu Asp Asp Ser Leu Val Ser Ile Phe Gly Asn Arg
 165 170 175

Arg Leu Lys Arg Phe Ser Met Val Val Gln Asp Gly Ile Val Lys Ala
 180 185 190

Leu Asn Val Glu Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro
 195 200 205

Asn Ile Ile Ser Gln Leu
 210

<210> 41
 <211> 1874
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (7)..(678)
 <223>

<400> 41
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 Met Ala Ala Gly Asp Gly Asp Val Lys Leu Gly Thr Leu Gly
 1 5 10

agt ggc agc gag agc agc aac gac ggc ggc agc gag agt cca ggc gac 96
 Ser Gly Ser Glu Ser Ser Asn Asp Gly Gly Ser Glu Ser Pro Gly Asp
 15 20 25 30

gcg gga gcg gca gcg gaa ggg gga ggc tgg gcg gcg gcg gcg ttg gcg 144
 Ala Gly Ala Ala Ala Glu Gly Gly Gly Trp Ala Ala Ala Ala Leu Ala
 35 40 45

ctt ctg acg ggg ggc ggg gaa atg ctg ctg aac gtg gcg ctg gtg gct 192
 Leu Leu Thr Gly Gly Gly Glu Met Leu Leu Asn Val Ala Leu Val Ala
 50 55 60

ctg gtg ctg ctg ggg gcc tac cgg ctg tgg gtg cgc tgg ggg cgg cgg 240
 Leu Val Leu Leu Gly Ala Tyr Arg Leu Trp Val Arg Trp Gly Arg Arg
 65 70 75

ggt ctg ggg gcc ggg gcc ggg gcg ggc gag gag agc ccc gcc acc tct Gly Leu Gly Ala Gly Ala Gly Ala Gly Glu Glu Ser Pro Ala Thr Ser 80 85 90	288
ctg cct cgc atg aag aag cgg gac ttc agc ttg gag cag ctg cgc cag Leu Pro Arg Met Lys Lys Arg Asp Phe Ser Leu Glu Gln Leu Arg Gln 95 100 105 110	336
tac gac ggc tcc cgc aac ccg cgc atc ctg ctc gcg gtc aat ggg aaa Tyr Asp Gly Ser Arg Asn Pro Arg Ile Leu Leu Ala Val Asn Gly Lys 115 120 125	384
gtc ttc gac gtg acc aaa ggc agc aag ttc tac ggc ccg gcg ggt cca Val Phe Asp Val Thr Lys Gly Ser Lys Phe Tyr Gly Pro Ala Gly Pro 130 135 140	432
tat gga ata ttt gct ggt agg gat gcc tcc aga gga ctg gcc aca ttt Tyr Gly Ile Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe 145 150 155	480
tgc cta gat aaa gat gca ctt aga gat gaa tat gat gat ctc tca gat Cys Leu Asp Lys Asp Ala Leu Arg Asp Glu Tyr Asp Asp Leu Ser Asp 160 165 170	528
ttg aat gca gta caa atg gag agt gtt cga gaa tgg gaa atg cag ttt Leu Asn Ala Val Gln Met Glu Ser Val Arg Glu Trp Glu Met Gln Phe 175 180 185 190	576
aaa gaa aaa tat gat tat gta ggc aga ctc cta aaa cca gga gaa gaa Lys Glu Lys Tyr Asp Tyr Val Gly Arg Leu Leu Lys Pro Gly Glu Glu 195 200 205	624
cca tca gaa tat aca gat gaa gaa gat acc aag gat cac aat aaa cag Pro Ser Glu Tyr Thr Asp Glu Glu Asp Thr Lys Asp His Asn Lys Gln 210 215 220	672
gat tga actttgtaaa caaccaaagt caggggcctt cagaactgca attcttactc Asp	728
cctttcacag actgtccgga gtctttgggt ttgattcacc tgctgcgaaa aacattcaac	788
aaattgtgta caagataaat taatctcact atgaagattt gaataactag acattattta	848
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aaagaaggag acagggattt ttttaaagag caagaaagtc acaatattac ttctttcctt	968
ccttttttcc ttctttcctt tcttctttct ctttctttct ttttaaaata tattgaagac	1028

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gcttttctgt tttcaaaaaa attgaaaaac aaatcaactc ttatccccaa cagctgccta 1688
attttaggag tctgaccctc cacatctcac tgggtgtgggt gcatggggct gtggagtggg 1748
tgtcagtatg gatgtgtctg aatgtgtgag gccttggaag ggactctttc tgcagatact 1808
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aaaaaa 1874

<210> 42
<211> 223
<212> PRT
<213> Homo sapiens

<400> 42

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Ser Glu Ser Ser Asn Asp Gly Gly Ser Glu Ser Pro Gly Asp Ala Gly
20 25 30

Ala Ala Ala Glu Gly Gly Gly Trp Ala Ala Ala Ala Leu Ala Leu Leu
35 40 45

Thr Gly Gly Gly Glu Met Leu Leu Asn Val Ala Leu Val Ala Leu Val
50 55 60

Leu Leu Gly Ala Tyr Arg Leu Trp Val Arg Trp Gly Arg Arg Gly Leu
65 70 75 80

Gly Ala Gly Ala Gly Ala Gly Glu Glu Ser Pro Ala Thr Ser Leu Pro
85 90 95

Arg Met Lys Lys Arg Asp Phe Ser Leu Glu Gln Leu Arg Gln Tyr Asp
100 105 110

Gly Ser Arg Asn Pro Arg Ile Leu Leu Ala Val Asn Gly Lys Val Phe
115 120 125

Asp Val Thr Lys Gly Ser Lys Phe Tyr Gly Pro Ala Gly Pro Tyr Gly
130 135 140

Ile Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe Cys Leu
145 150 155 160

Asp Lys Asp Ala Leu Arg Asp Glu Tyr Asp Asp Leu Ser Asp Leu Asn
165 170 175

Ala Val Gln Met Glu Ser Val Arg Glu Trp Glu Met Gln Phe Lys Glu
180 185 190

Lys Tyr Asp Tyr Val Gly Arg Leu Leu Lys Pro Gly Glu Glu Pro Ser
195 200 205

Glu Tyr Thr Asp Glu Glu Asp Thr Lys Asp His Asn Lys Gln Asp
210 215 220

<210> 43
<211> 3795
<212> DNA
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<220>

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<222> (236)..(1633)

<223>

<400> 43

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cggcccaagc ccgaccccggt gtcccctcct cggccgcccc ccgcccggcc gcccgccctc 180

gggcctcccc ccgggccctc ggtcccctcc cccgctggcg gggcccggac agaag atg 238
Met
1

gtg cag aag aaa cca gcc gaa ctt cag ggt ttc cac cgt tcg ttc aag 286
Val Gln Lys Lys Pro Ala Glu Leu Gln Gly Phe His Arg Ser Phe Lys
5 10 15

ggg cag aac ccc ttc gag ctg gcc ttc tcc cta gac cag ccc gac cac 334
Gly Gln Asn Pro Phe Glu Leu Ala Phe Ser Leu Asp Gln Pro Asp His
20 25 30

gga gac tct gac ttt ggc ctg cag tgc tca gcc cgc cct gac atg ccc 382
Gly Asp Ser Asp Phe Gly Leu Gln Cys Ser Ala Arg Pro Asp Met Pro
35 40 45

gcc agc cag ccc att gac atc ccg gac gcc aag aag agg ggc aag aag 430
Ala Ser Gln Pro Ile Asp Ile Pro Asp Ala Lys Lys Arg Gly Lys Lys
50 55 60 65

aag aag cgc ggc cgg gcc acc gac agc ttc tcg ggc agg ttt gaa gac 478
Lys Lys Arg Gly Arg Ala Thr Asp Ser Phe Ser Gly Arg Phe Glu Asp
70 75 80

gtc tac cag ctg cag gaa gat gtg ctg ggg gag ggc gct cat gcc cga 526
Val Tyr Gln Leu Gln Glu Asp Val Leu Gly Glu Gly Ala His Ala Arg
85 90 95

gtg cag acc tgc atc aac ctg atc acc agc cag gag tac gcc gtc aag 574
Val Gln Thr Cys Ile Asn Leu Ile Thr Ser Gln Glu Tyr Ala Val Lys
100 105 110

atc att gag aag cag cca ggc cac att cgg agc agg gtt ttc agg gag 622
Ile Ile Glu Lys Gln Pro Gly His Ile Arg Ser Arg Val Phe Arg Glu
115 120 125

gtg gag atg ctg tac cag tgc cag gga cac agg aac gtc cta gag ctg 670
Val Glu Met Leu Tyr Gln Cys Gln Gly His Arg Asn Val Leu Glu Leu
119/201

130	135	140	145	
att gag ttc ttc gag gag gag gac cgc ttc tac ctg gtg ttt gag aag				718
Ile Glu Phe Phe Glu Glu Glu Asp Arg Phe Tyr Leu Val Phe Glu Lys				
	150	155	160	
atg cgg gga ggc tcc atc ctg agc cac atc cac aag cgc cgg cac ttc				766
Met Arg Gly Gly Ser Ile Leu Ser His Ile His Lys Arg Arg His Phe				
	165	170	175	
aac gag ctg gag gcc agc gtg gtg gtg cag gac gtg gcc agc gcc ttg				814
Asn Glu Leu Glu Ala Ser Val Val Val Gln Asp Val Ala Ser Ala Leu				
	180	185	190	
gac ttt ctg cat aac aaa ggc atc gcc cac agg gac cta aag ccg gaa				862
Asp Phe Leu His Asn Lys Gly Ile Ala His Arg Asp Leu Lys Pro Glu				
	195	200	205	
aac atc ctc tgt gag cac ccc aac cag gtc tcc ccc gtg aag atc tgt				910
Asn Ile Leu Cys Glu His Pro Asn Gln Val Ser Pro Val Lys Ile Cys				
	210	215	220	225
gac ttc gac ctg ggc agc ggc atc aaa ctc aac ggg gac tgc tcc cct				958
Asp Phe Asp Leu Gly Ser Gly Ile Lys Leu Asn Gly Asp Cys Ser Pro				
	230	235	240	
atc tcc acc ccg gag ctg ctc act ccg tgc ggc tgc gcg gag tac atg				1006
Ile Ser Thr Pro Glu Leu Leu Thr Pro Cys Gly Ser Ala Glu Tyr Met				
	245	250	255	
gcc ccg gag gta gtg gag gcc ttc agc gag gag gct agc atc tac gac				1054
Ala Pro Glu Val Val Glu Ala Phe Ser Glu Glu Ala Ser Ile Tyr Asp				
	260	265	270	
aag cgc tgc gac ctg tgg agc ctg ggc gtc atc ttg tat atc cta ctc				1102
Lys Arg Cys Asp Leu Trp Ser Leu Gly Val Ile Leu Tyr Ile Leu Leu				
	275	280	285	
agc ggc tac ccg ccc ttc gtg ggc cgc tgt ggc agc gac tgc ggc tgg				1150
Ser Gly Tyr Pro Pro Phe Val Gly Arg Cys Gly Ser Asp Cys Gly Trp				
	290	295	300	305
gac cgc ggc gag gcc tgc cct gcc tgc cag aac atg ctg ttt gag agc				1198
Asp Arg Gly Glu Ala Cys Pro Ala Cys Gln Asn Met Leu Phe Glu Ser				
	310	315	320	
atc cag gag ggc aag tac gag ttc ccc gac aag gac tgg gcc cac atc				1246
Ile Gln Glu Gly Lys Tyr Glu Phe Pro Asp Lys Asp Trp Ala His Ile				
	325	330	335	

tcc tgc gct gcc aaa gac ctc atc tcc aag ctg ctg gtc cgt gac gcc Ser Cys Ala Ala Lys Asp Leu Ile Ser Lys Leu Leu Val Arg Asp Ala 340 345 350	1294
aag cag agg ctg agt gcc gcc caa gtc ctg cag cac ccc tgg gtt cag Lys Gln Arg Leu Ser Ala Ala Gln Val Leu Gln His Pro Trp Val Gln 355 360 365	1342
ggg tgc gcc ccg gag aac acc ttg ccc act ccc atg gtc ctg cag agg Gly Cys Ala Pro Glu Asn Thr Leu Pro Thr Pro Met Val Leu Gln Arg 370 375 380 385	1390
aac agc tgt gcc aaa gac ctc acg tcc ttc gcg gct gag gcc att gcc Asn Ser Cys Ala Lys Asp Leu Thr Ser Phe Ala Ala Glu Ala Ile Ala 390 395 400	1438
atg aac cgg cag ctg gcc cag cac gac gag gac ctg gct gag gag gag Met Asn Arg Gln Leu Ala Gln His Asp Glu Asp Leu Ala Glu Glu Glu 405 410 415	1486
gcc gcg ggg cag ggc cag ccc gtc ctg gtc cga gct acc tca cgc tgc Ala Ala Gly Gln Gly Gln Pro Val Leu Val Arg Ala Thr Ser Arg Cys 420 425 430	1534
ctg cag ctg tct cca ccc tcc cag tcc aag ctg gcg cag cgg cgg caa Leu Gln Leu Ser Pro Pro Ser Gln Ser Lys Leu Ala Gln Arg Arg Gln 435 440 445	1582
agg gcc agt ctg tcc tcg gcc cca gtg gtc ctg gtg gga gac cac gcc Arg Ala Ser Leu Ser Ser Ala Pro Val Val Leu Val Gly Asp His Ala 450 455 460 465	1630
tga ccctcccatc tcccctctgt acataggtca cccgtccccc aatcaaattct	1683
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aaaaaaaaaa aa 3795

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<212> PRT
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Lys Gly Gln Asn Pro Phe Glu Leu Ala Phe Ser Leu Asp Gln Pro Asp
20 25 30

His Gly Asp Ser Asp Phe Gly Leu Gln Cys Ser Ala Arg Pro Asp Met
35 40 45

Pro Ala Ser Gln Pro Ile Asp Ile Pro Asp Ala Lys Lys Arg Gly Lys
50 55 60

Lys Lys Lys Arg Gly Arg Ala Thr Asp Ser Phe Ser Gly Arg Phe Glu
65 70 75 80

Asp Val Tyr Gln Leu Gln Glu Asp Val Leu Gly Glu Gly Ala His Ala
85 90 95

Arg Val Gln Thr Cys Ile Asn Leu Ile Thr Ser Gln Glu Tyr Ala Val
100 105 110

Lys Ile Ile Glu Lys Gln Pro Gly His Ile Arg Ser Arg Val Phe Arg
115 120 125

Glu Val Glu Met Leu Tyr Gln Cys Gln Gly His Arg Asn Val Leu Glu
130 135 140

Leu Ile Glu Phe Phe Glu Glu Glu Asp Arg Phe Tyr Leu Val Phe Glu
145 150 155 160

Lys Met Arg Gly Gly Ser Ile Leu Ser His Ile His Lys Arg Arg His
165 170 175

Phe Asn Glu Leu Glu Ala Ser Val Val Val Gln Asp Val Ala Ser Ala
180 185 190

Leu Asp Phe Leu His Asn Lys Gly Ile Ala His Arg Asp Leu Lys Pro
195 200 205

Glu Asn Ile Leu Cys Glu His Pro Asn Gln Val Ser Pro Val Lys Ile
210 215 220

Cys Asp Phe Asp Leu Gly Ser Gly Ile Lys Leu Asn Gly Asp Cys Ser
225 230 235 240

Pro Ile Ser Thr Pro Glu Leu Leu Thr Pro Cys Gly Ser Ala Glu Tyr
245 250 255

Met Ala Pro Glu Val Val Glu Ala Phe Ser Glu Glu Ala Ser Ile Tyr
260 265 270

Asp Lys Arg Cys Asp Leu Trp Ser Leu Gly Val Ile Leu Tyr Ile Leu
275 280 285

Leu Ser Gly Tyr Pro Pro Phe Val Gly Arg Cys Gly Ser Asp Cys Gly
290 295 300

Trp Asp Arg Gly Glu Ala Cys Pro Ala Cys Gln Asn Met Leu Phe Glu
305 310 315 320

Ser Ile Gln Glu Gly Lys Tyr Glu Phe Pro Asp Lys Asp Trp Ala His
325 330 335

Ile Ser Cys Ala Ala Lys Asp Leu Ile Ser Lys Leu Leu Val Arg Asp
340 345 350

Ala Lys Gln Arg Leu Ser Ala Ala Gln Val Leu Gln His Pro Trp Val
 355 360 365

Gln Gly Cys Ala Pro Glu Asn Thr Leu Pro Thr Pro Met Val Leu Gln
 370 375 380

Arg Asn Ser Cys Ala Lys Asp Leu Thr Ser Phe Ala Ala Glu Ala Ile
 385 390 395 400

Ala Met Asn Arg Gln Leu Ala Gln His Asp Glu Asp Leu Ala Glu Glu
 405 410 415

Glu Ala Ala Gly Gln Gly Gln Pro Val Leu Val Arg Ala Thr Ser Arg
 420 425 430

Cys Leu Gln Leu Ser Pro Pro Ser Gln Ser Lys Leu Ala Gln Arg Arg
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Gln Arg Ala Ser Leu Ser Ser Ala Pro Val Val Leu Val Gly Asp His
 450 455 460

Ala
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 catctgggag gtgaggggca cttctgccgg gccgccccta ctgggaagtg aggagcccct 180
 ctgcccggcc acgaccccgt ctgggaggtg tgcccagcgg ctcatctgggg atgggccatg 240
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cggatggttg cggggtctgt gtggatagaa gtagacatgg gagacttttc attttgttct	360
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tgtgctctct gaaacatgtg ctgtgtccac tcagggttaa atggattaag ggcggtgcaa	480
gatgtgcttt gttaaacaga tgcttgaagg cagcatgctc gttaagagtc atcaccactc	540
cctaattctta agtaccagg gacacaaaca ctgcggaagg ccgcagggtc ctctgcctag	600
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 <213> Homo sapiens

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cggccctact gggaagtgaag gagccccctc gcccgccag ccgccccgtc cgggagggag	180
gtgggggggt cagccgcccgc ccgtccggga cctagctggg caccgatggg ccggcacggg	240
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cgagcaaagg tagtgccgag tgccagtaca tgatgccatc ctacagacgat gggaggcggg	360
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cccgtggtta tgcggagccg ccgcattcct tagcgatcgc ggggcagccg ccgctgccgc	180
cgtgggagac tgacgcagcg cgggcgcgtg gagccgccgc cgccccctccc ccaccgccgc	240
tctcgcgcca gccggtcccc gcgtgccgcg cccttctccc cggccgcacc cgagacctcg	300
cgcgcgcgcg ctgccacgcg cccccccac cgccgccgcc gccccagccc cgcgccaccg	360
ccccagcccc cccagccccg aggtcccgcg tggagctgcc gccgccgccg gggagaagg	419
atg aag gac aaa cag aag aag aag aag gag cgc acg tgg gcc gag gcc	467
Met Lys Asp Lys Gln Lys Lys Lys Lys Glu Arg Thr Trp Ala Glu Ala	
1 5 10 15	
gcg cgc ctg gta tta gaa aac tac tcg gat gct cca atg aca cca aaa	515
Ala Arg Leu Val Leu Glu Asn Tyr Ser Asp Ala Pro Met Thr Pro Lys	
20 25 30	
cag att ctg cag gtc ata gag gca gaa gga cta aag gaa atg aga agt	563
Gln Ile Leu Gln Val Ile Glu Ala Glu Gly Leu Lys Glu Met Arg Ser	
35 40 45	
ggg act tcc cct ctc gca tgc ctc aat gct atg cta cat tcc aat tca	611
Gly Thr Ser Pro Leu Ala Cys Leu Asn Ala Met Leu His Ser Asn Ser	
50 55 60	
aga gga gga gag ggg ttg ttt tat aaa ctg cct ggc cga atc agc ctt	659
Arg Gly Gly Glu Gly Leu Phe Tyr Lys Leu Pro Gly Arg Ile Ser Leu	
65 70 75 80	
ttc acg ctc aag aag gat gcc ctg cag tgg tct cgc cat cca gct aca	707
Phe Thr Leu Lys Lys Asp Ala Leu Gln Trp Ser Arg His Pro Ala Thr	
85 90 95	
gtg gag gga gag gag cca gag gac acg gct gat gtg gag agc tgt ggg	755
Val Glu Gly Glu Glu Pro Glu Asp Thr Ala Asp Val Glu Ser Cys Gly	
100 105 110	
tct aat gaa gcc agc act gtg agt ggt gaa aac gat gta tct ctt gat	803
Ser Asn Glu Ala Ser Thr Val Ser Gly Glu Asn Asp Val Ser Leu Asp	
115 120 125	
gaa aca tct tcg aac gca tcc tgt tct aca gaa tct cag agt cga cct	851
Glu Thr Ser Ser Asn Ala Ser Cys Ser Thr Glu Ser Gln Ser Arg Pro	
130 135 140	
ctt tcc aat ccc agg gac agc tac aga gct tcc tca cag gcg aac aaa	899
Leu Ser Asn Pro Arg Asp Ser Tyr Arg Ala Ser Ser Gln Ala Asn Lys	
145 150 155 160	

caa aag aaa aag act ggg gtg atg ctg cct cga gtt gtc ctg act cct Gln Lys Lys Lys Thr Gly Val Met Leu Pro Arg Val Val Leu Thr Pro 165 170 175	947
ctg aag gta aac ggg gcc cac gtg gaa tct gca tca ggg ttc tcg ggc Leu Lys Val Asn Gly Ala His Val Glu Ser Ala Ser Gly Phe Ser Gly 180 185 190	995
tgc cac gcc gat ggc gag agc ggc agc ccg tcc agc agc agc agc ggc Cys His Ala Asp Gly Glu Ser Gly Ser Pro Ser Ser Ser Ser Ser Gly 195 200 205	1043
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cag gac cct gcc ccg ctc ctg aga ggc ttc cgg aag cca gcc aca ggt Gln Asp Pro Ala Pro Leu Leu Arg Gly Phe Arg Lys Pro Ala Thr Gly 225 230 235 240	1139
caa atg aag cgc aac aga ggg gaa gaa ata gat ttt gag aca cct ggg Gln Met Lys Arg Asn Arg Gly Glu Glu Ile Asp Phe Glu Thr Pro Gly 245 250 255	1187
tcc att ctt gtc aac acc aac ctc cgt gcc ctg atc aac tct cgg acc Ser Ile Leu Val Asn Thr Asn Leu Arg Ala Leu Ile Asn Ser Arg Thr 260 265 270	1235
ttc cat gcc tta cca tca cac ttc cag cag cag ctc ctc ttc ctc ctg Phe His Ala Leu Pro Ser His Phe Gln Gln Gln Leu Leu Phe Leu Leu 275 280 285	1283
cct gaa gta gac aga cag gtg ggg acg gat ggc ctg ttg cgt ctc agc Pro Glu Val Asp Arg Gln Val Gly Thr Asp Gly Leu Leu Arg Leu Ser 290 295 300	1331
agc agt gca cta aat aac gag ttt ttt acc cat gcg gct cag agc tgg Ser Ser Ala Leu Asn Asn Glu Phe Phe Thr His Ala Ala Gln Ser Trp 305 310 315 320	1379
cgg gag cgc ctg gct gat ggt gaa ttt act cat gag atg caa gtc agg Arg Glu Arg Leu Ala Asp Gly Glu Phe Thr His Glu Met Gln Val Arg 325 330 335	1427
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Lys Phe Phe Glu Asp Tyr Tyr Gly Gln Lys Leu Gly Leu Thr Lys Glu	
355 360 365	
gag tca ttg cag cag aac gtg ggc cag gag gag gct gaa atc aaa agt	1571
Glu Ser Leu Gln Gln Asn Val Gly Gln Glu Glu Ala Glu Ile Lys Ser	
370 375 380	
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Gly Leu Cys Val Pro Gly Glu Ser Val Arg Ile Gln Arg Gly Pro Ala	
385 390 395 400	
acc cga cag cga gat ggg cat ttt aag aaa cgc tct cgg cca gat ctc	1667
Thr Arg Gln Arg Asp Gly His Phe Lys Lys Arg Ser Arg Pro Asp Leu	
405 410 415	
cga acc aga gcc aga agg aat ctg tac aaa aaa cag gag tca gaa caa	1715
Arg Thr Arg Ala Arg Arg Asn Leu Tyr Lys Lys Gln Glu Ser Glu Gln	
420 425 430	
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Ala Gly Val Ala Lys Asp Ala Lys Ser Val Ala Ser Asp Val Pro Leu	
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tac aag gat ggg gag gct aag act gac cca gca ggg ctg agc agt ccc	1811
Tyr Lys Asp Gly Glu Ala Lys Thr Asp Pro Ala Gly Leu Ser Ser Pro	
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cat ctg cca ggc aca tcc tct gca gca ccc gac ctg gag ggt ccc gaa	1859
His Leu Pro Gly Thr Ser Ser Ala Ala Pro Asp Leu Glu Gly Pro Glu	
465 470 475 480	
ttc cca gtt gag tct gtg gct tct cgg atc cag gct gag cca gac aac	1907
Phe Pro Val Glu Ser Val Ala Ser Arg Ile Gln Ala Glu Pro Asp Asn	
485 490 495	
ttg gca cgt gcc tct gca tct cca gac aga att cct agc ctg cct cag	1955
Leu Ala Arg Ala Ser Ala Ser Pro Asp Arg Ile Pro Ser Leu Pro Gln	
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gaa act gtg gat cag gaa ccc aag gat cag aag agg aaa tcc ttt gag	2003
Glu Thr Val Asp Gln Glu Pro Lys Asp Gln Lys Arg Lys Ser Phe Glu	
515 520 525	
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Gln Ala Ala Ser Ala Ser Phe Pro Glu Lys Lys Pro Arg Leu Glu Asp	
530 535 540	
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Arg Gln Ser Phe Arg Asn Thr Ile Glu Ser Val His Thr Glu Lys Pro	
545 550 555 560	

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cga ggg gcg aga ggt cac cac tgc cat aga gag gcg gcc acc act gcc Arg Gly Ala Arg Gly His His Cys His Arg Glu Ala Ala Thr Thr Ala 625 630 635 640	2339
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gag gga ggt ggc aga ggc agc agc agt ggt gat ggt ggt gag gcc tgt Glu Gly Gly Gly Arg Gly Ser Ser Ser Gly Asp Gly Gly Glu Ala Cys 660 665 670	2435
ggc cac cct gag ccc agg gga ggc ccg agc acc cct gga aag tgt acg Gly His Pro Glu Pro Arg Gly Gly Pro Ser Thr Pro Gly Lys Cys Thr 675 680 685	2483
tca gat cta cag cga aca caa cta ctg ccg cct tat cct cta aat ggg Ser Asp Leu Gln Arg Thr Gln Leu Leu Pro Pro Tyr Pro Leu Asn Gly 690 695 700	2531
gag cat acc cag gcc gga act gcc atg tcc aga gct agg aga gag gac Glu His Thr Gln Ala Gly Thr Ala Met Ser Arg Ala Arg Arg Glu Asp 705 710 715 720	2579
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ccc act ggg gac cag cca tgc cag gcc ttg ccc cta ctg tcc tcc caa	2723

Pro Thr Gly Asp Gln Pro Cys Gln Ala Leu Pro Leu Leu Ser Ser Gln	
755 760 765	
acc tca gta gct gag aga tta gtg gag cag cct cag ttg cat ccg gat	2771
Thr Ser Val Ala Glu Arg Leu Val Glu Gln Pro Gln Leu His Pro Asp	
770 775 780	
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Val Arg Thr Glu Cys Glu Ser Gly Thr Thr Ser Trp Glu Ser Asp Asp	
785 790 795 800	
gag gag caa gga ccc acc gtt cct gca gac aat ggt ccc att ccg tct	2867
Glu Glu Gln Gly Pro Thr Val Pro Ala Asp Asn Gly Pro Ile Pro Ser	
805 810 815	
cta gtg gga gat gat aca tta gag aaa gga act ggc caa gct ctt gac	2915
Leu Val Gly Asp Asp Thr Leu Glu Lys Gly Thr Gly Gln Ala Leu Asp	
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agt cat ccc act atg aag gat cct gta aat gtg acc ccc agt tcc aca	2963
Ser His Pro Thr Met Lys Asp Pro Val Asn Val Thr Pro Ser Ser Thr	
835 840 845	
cct gaa tcc tca ccg act gat tgc ctg cag aac aga gca ttt gat gac	3011
Pro Glu Ser Ser Pro Thr Asp Cys Leu Gln Asn Arg Ala Phe Asp Asp	
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Glu Leu Gly Leu Gly Gly Ser Cys Pro Pro Met Arg Glu Ser Asp Thr	
865 870 875 880	
aga caa gaa aac ttg aaa acc aag gct ctc gtt tct aac agt tct ttg	3107
Arg Gln Glu Asn Leu Lys Thr Lys Ala Leu Val Ser Asn Ser Ser Leu	
885 890 895	
cat tgg ata ccc atc cca tcg aat gat gag gta gtg aaa cag ccc aaa	3155
His Trp Ile Pro Ile Pro Ser Asn Asp Glu Val Val Lys Gln Pro Lys	
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cca gaa tcc aga gaa cac ata cca tct gtt gag ccc cag gtt gga gag	3203
Pro Glu Ser Arg Glu His Ile Pro Ser Val Glu Pro Gln Val Gly Glu	
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Glu Trp Glu Lys Ala Ala Pro Thr Pro Pro Ala Leu Pro Gly Asp Leu	
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Thr Ala Glu Glu Gly Leu Asp Pro Leu Asp Ser Leu Thr Ser Leu Trp	
945 950 955 960	

act gtg cca tct cga gga ggc agt gac agc aat ggc agt tac tgt caa	3347
Thr Val Pro Ser Arg Gly Gly Ser Asp Ser Asn Gly Ser Tyr Cys Gln	
965 970 975	
cag gtg gac att gaa aag ctg aaa atc aac gga gac tct gaa gca ctg	3395
Gln Val Asp Ile Glu Lys Leu Lys Ile Asn Gly Asp Ser Glu Ala Leu	
980 985 990	
agt cct cac ggt gag tcc acg gat aca gcc tct gac ttt gaa ggt cac	3443
Ser Pro His Gly Glu Ser Thr Asp Thr Ala Ser Asp Phe Glu Gly His	
995 1000 1005	
ctc acg gag gac agc agt gag gct gac act aga gaa gct gca gtg	3488
Leu Thr Glu Asp Ser Ser Glu Ala Asp Thr Arg Glu Ala Ala Val	
1010 1015 1020	
aca aag gga tct tcg gtg gac aag gat gag aaa ccc aat tgg aac	3533
Thr Lys Gly Ser Ser Val Asp Lys Asp Glu Lys Pro Asn Trp Asn	
1025 1030 1035	
caa tct gcc cca ctg tcc aag gtg aat ggt gac atg cgt ctg gtt	3578
Gln Ser Ala Pro Leu Ser Lys Val Asn Gly Asp Met Arg Leu Val	
1040 1045 1050	
aca agg aca gat ggg atg gtt gct cct cag agc tgg gtg tct cga	3623
Thr Arg Thr Asp Gly Met Val Ala Pro Gln Ser Trp Val Ser Arg	
1055 1060 1065	
gta tgt gcg gtc cgc caa aag atc cca gat tcc cta ctg ctg gcc	3668
Val Cys Ala Val Arg Gln Lys Ile Pro Asp Ser Leu Leu Leu Ala	
1070 1075 1080	
agt act gag tac cag cca aga gcc gtg tgc ctg tcc atg cct ggg	3713
Ser Thr Glu Tyr Gln Pro Arg Ala Val Cys Leu Ser Met Pro Gly	
1085 1090 1095	
tcc tca gtg gag gcc act aac cca ctt gtg atg cag ttg ctg cag	3758
Ser Ser Val Glu Ala Thr Asn Pro Leu Val Met Gln Leu Leu Gln	
1100 1105 1110	
ggt agc ttg ccc cta gag aag gtt ctt cca cca gcc cac gat gac	3803
Gly Ser Leu Pro Leu Glu Lys Val Leu Pro Pro Ala His Asp Asp	
1115 1120 1125	
agc atg tca gaa tcc cca caa gta cca ctt aca aaa gac cag agc	3848
Ser Met Ser Glu Ser Pro Gln Val Pro Leu Thr Lys Asp Gln Ser	
1130 1135 1140	
cat ggc tcg cta cgc atg gga tct tta cat ggt ctt gga aaa aac	3893
132/201	

His Gly Ser Leu Arg Met Gly Ser Leu His Gly Leu Gly Lys Asn	
1145 1150 1155	
agt ggc atg gtt gat gga agc agc ccc agt tct tta agg gct ttg	3938
Ser Gly Met Val Asp Gly Ser Ser Pro Ser Ser Leu Arg Ala Leu	
1160 1165 1170	
aag gag cct ctt ctg cca gat agc tgt gaa aca ggc act ggt ctt	3983
Lys Glu Pro Leu Leu Pro Asp Ser Cys Glu Thr Gly Thr Gly Leu	
1175 1180 1185	
gcc agg att gag gcc acc cag gct cct gga gca ccc caa aag aat	4028
Ala Arg Ile Glu Ala Thr Gln Ala Pro Gly Ala Pro Gln Lys Asn	
1190 1195 1200	
tgc aag gca gtc cca agt ttt gac tcc ctc cat cca gtg aca aat	4073
Cys Lys Ala Val Pro Ser Phe Asp Ser Leu His Pro Val Thr Asn	
1205 1210 1215	
ccc att aca tcc tct agg aaa ctg gaa gaa atg gat tcc aaa gag	4118
Pro Ile Thr Ser Ser Arg Lys Leu Glu Glu Met Asp Ser Lys Glu	
1220 1225 1230	
cag ttc tct tcc ttt agt tgt gaa gat cag aag gaa gtc cgt gct	4163
Gln Phe Ser Ser Phe Ser Cys Glu Asp Gln Lys Glu Val Arg Ala	
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atg tca cag gac agt aat tca aat gct gct cca gga aag agc cca	4208
Met Ser Gln Asp Ser Asn Ser Asn Ala Ala Pro Gly Lys Ser Pro	
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gga gat ctt act acc tcg aga aca cct cgt ttc tca tct cca aat	4253
Gly Asp Leu Thr Thr Ser Arg Thr Pro Arg Phe Ser Ser Pro Asn	
1265 1270 1275	
gtg atc tcc ttt ggt cca gag cag aca ggt cgg gcc ctg ggt gat	4298
Val Ile Ser Phe Gly Pro Glu Gln Thr Gly Arg Ala Leu Gly Asp	
1280 1285 1290	
cag agc aat gtt aca ggc caa ggg aag aag ctt ttt ggc tct ggg	4343
Gln Ser Asn Val Thr Gly Gln Gly Lys Lys Leu Phe Gly Ser Gly	
1295 1300 1305	
aat gtg gct gca acc ctt cag cgc ccc agg cct gcg gac ccg atg	4388
Asn Val Ala Ala Thr Leu Gln Arg Pro Arg Pro Ala Asp Pro Met	
1310 1315 1320	
cct ctt cct gct gag atc cct cca gtt ttt ccc agt ggg aag ttg	4433
Pro Leu Pro Ala Glu Ile Pro Pro Val Phe Pro Ser Gly Lys Leu	
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gga cca agc aca aac tcc atg tct ggt ggg gta cag act cca agg Gly Pro Ser Thr Asn Ser Met Ser Gly Gly Val Gln Thr Pro Arg 1340 1345 1350	4478
gaa gac tgg gct cca aag cca cat gcc ttt gtt ggc agc gtc aag Glu Asp Trp Ala Pro Lys Pro His Ala Phe Val Gly Ser Val Lys 1355 1360 1365	4523
aat gag aag act ttt gtg ggg ggt cct ctt aag gca aat gcc gag Asn Glu Lys Thr Phe Val Gly Gly Pro Leu Lys Ala Asn Ala Glu 1370 1375 1380	4568
aac agg aaa gct act ggg cat agt ccc ctg gaa ctg gtg ggt cac Asn Arg Lys Ala Thr Gly His Ser Pro Leu Glu Leu Val Gly His 1385 1390 1395	4613
ttg gaa ggg atg ccc ttt gtc atg gac ttg ccc ttc tgg aaa tta Leu Glu Gly Met Pro Phe Val Met Asp Leu Pro Phe Trp Lys Leu 1400 1405 1410	4658
ccc cga gag cca ggg aag ggg ctc agt gag cct ctg gag cct tct Pro Arg Glu Pro Gly Lys Gly Leu Ser Glu Pro Leu Glu Pro Ser 1415 1420 1425	4703
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ctt tct aaa ctc caa ctg agt tcc acc agc ttt aat tat tcc tct Leu Ser Lys Leu Gln Leu Ser Ser Thr Ser Phe Asn Tyr Ser Ser 1445 1450 1455	4793
agc tct ccc acc ttt ccc aaa ggc ctt gct gga agt gtg gtg cag Ser Ser Pro Thr Phe Pro Lys Gly Leu Ala Gly Ser Val Val Gln 1460 1465 1470	4838
ctg agc cac aaa gca aac ttt ggt gcg agc cac agt gca tca ctt Leu Ser His Lys Ala Asn Phe Gly Ala Ser His Ser Ala Ser Leu 1475 1480 1485	4883
tcc ttg caa atg ttc act gac agc agc acg gtg gaa agc atc tcg Ser Leu Gln Met Phe Thr Asp Ser Ser Thr Val Glu Ser Ile Ser 1490 1495 1500	4928
ctc cag tgt gcg tgc agc ctg aaa gcc atg atc atg tgc caa ggc Leu Gln Cys Ala Cys Ser Leu Lys Ala Met Ile Met Cys Gln Gly 1505 1510 1515	4973
tgc ggt gcg ttc tgt cac gat gac tgt att gga ccc tca aag ctc 134/201	5018

Cys Gly Ala Phe Cys His Asp Asp Cys Ile Gly Pro Ser Lys Leu
1520 1525 1530

tgt gta ttg tgc ctt gtg gtg aga taa taaattatgg ccatgggaaa 5065
Cys Val Leu Cys Leu Val Val Arg
1535 1540

cattgtatat ttagtgtgtg tattttgata atgattgac ttaaactctgt atacagaata 5125
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tgcttgctgc catatgtgac aaatcaccac caccagtgtt aagtgccttct ggattcatgg 6385

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aatttgtatg acttcaagtc tcattttatc tgaaagggtt ttttctcatt taatctgatg 6745
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<213> Homo sapiens

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Ala Arg Leu Val Leu Glu Asn Tyr Ser Asp Ala Pro Met Thr Pro Lys
          20          25          30

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Gln Ile Leu Gln Val Ile Glu Ala Glu Gly Leu Lys Glu Met Arg Ser
          35          40          45

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Gly Thr Ser Pro Leu Ala Cys Leu Asn Ala Met Leu His Ser Asn Ser
          50          55          60

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Arg Gly Gly Glu Gly Leu Phe Tyr Lys Leu Pro Gly Arg Ile Ser Leu
65          70          75          80

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Phe Thr Leu Lys Lys Asp Ala Leu Gln Trp Ser Arg His Pro Ala Thr
85 90 95

Val Glu Gly Glu Glu Pro Glu Asp Thr Ala Asp Val Glu Ser Cys Gly
100 105 110

Ser Asn Glu Ala Ser Thr Val Ser Gly Glu Asn Asp Val Ser Leu Asp
115 120 125

Glu Thr Ser Ser Asn Ala Ser Cys Ser Thr Glu Ser Gln Ser Arg Pro
130 135 140

Leu Ser Asn Pro Arg Asp Ser Tyr Arg Ala Ser Ser Gln Ala Asn Lys
145 150 155 160

Gln Lys Lys Lys Thr Gly Val Met Leu Pro Arg Val Val Leu Thr Pro
165 170 175

Leu Lys Val Asn Gly Ala His Val Glu Ser Ala Ser Gly Phe Ser Gly
180 185 190

Cys His Ala Asp Gly Glu Ser Gly Ser Pro Ser Ser Ser Ser Ser Gly
195 200 205

Ser Leu Ala Leu Gly Ser Ala Ala Ile Arg Gly Gln Ala Glu Val Thr
210 215 220

Gln Asp Pro Ala Pro Leu Leu Arg Gly Phe Arg Lys Pro Ala Thr Gly
225 230 235 240

Gln Met Lys Arg Asn Arg Gly Glu Glu Ile Asp Phe Glu Thr Pro Gly
245 250 255

Ser Ile Leu Val Asn Thr Asn Leu Arg Ala Leu Ile Asn Ser Arg Thr
260 265 270

Phe His Ala Leu Pro Ser His Phe Gln Gln Gln Leu Leu Phe Leu Leu
137/201

275

280

285

Pro Glu Val Asp Arg Gln Val Gly Thr Asp Gly Leu Leu Arg Leu Ser
 290 295 300

Ser Ser Ala Leu Asn Asn Glu Phe Phe Thr His Ala Ala Gln Ser Trp
 305 310 315 320

Arg Glu Arg Leu Ala Asp Gly Glu Phe Thr His Glu Met Gln Val Arg
 325 330 335

Ile Arg Gln Glu Met Glu Lys Glu Lys Lys Val Glu Gln Trp Lys Glu
 340 345 350

Lys Phe Phe Glu Asp Tyr Tyr Gly Gln Lys Leu Gly Leu Thr Lys Glu
 355 360 365

Glu Ser Leu Gln Gln Asn Val Gly Gln Glu Glu Ala Glu Ile Lys Ser
 370 375 380

Gly Leu Cys Val Pro Gly Glu Ser Val Arg Ile Gln Arg Gly Pro Ala
 385 390 395 400

Thr Arg Gln Arg Asp Gly His Phe Lys Lys Arg Ser Arg Pro Asp Leu
 405 410 415

Arg Thr Arg Ala Arg Arg Asn Leu Tyr Lys Lys Gln Glu Ser Glu Gln
 420 425 430

Ala Gly Val Ala Lys Asp Ala Lys Ser Val Ala Ser Asp Val Pro Leu
 435 440 445

Tyr Lys Asp Gly Glu Ala Lys Thr Asp Pro Ala Gly Leu Ser Ser Pro
 450 455 460

His Leu Pro Gly Thr Ser Ser Ala Ala Pro Asp Leu Glu Gly Pro Glu
 465 470 475 480

Phe Pro Val Glu Ser Val Ala Ser Arg Ile Gln Ala Glu Pro Asp Asn
485 490 495

Leu Ala Arg Ala Ser Ala Ser Pro Asp Arg Ile Pro Ser Leu Pro Gln
500 505 510

Glu Thr Val Asp Gln Glu Pro Lys Asp Gln Lys Arg Lys Ser Phe Glu
515 520 525

Gln Ala Ala Ser Ala Ser Phe Pro Glu Lys Lys Pro Arg Leu Glu Asp
530 535 540

Arg Gln Ser Phe Arg Asn Thr Ile Glu Ser Val His Thr Glu Lys Pro
545 550 555 560

Gln Pro Thr Lys Glu Glu Pro Lys Val Pro Pro Ile Arg Ile Gln Leu
565 570 575

Ser Arg Ile Lys Pro Pro Trp Val Val Lys Gly Gln Pro Thr Tyr Gln
580 585 590

Ile Cys Pro Arg Ile Ile Pro Thr Thr Glu Ser Ser Cys Arg Gly Trp
595 600 605

Thr Gly Ala Arg Thr Leu Ala Asp Ile Lys Ala Arg Ala Leu Gln Val
610 615 620

Arg Gly Ala Arg Gly His His Cys His Arg Glu Ala Ala Thr Thr Ala
625 630 635 640

Ile Gly Gly Gly Gly Gly Pro Gly Gly Gly Gly Gly Gly Ala Thr Asp
645 650 655

Glu Gly Gly Gly Arg Gly Ser Ser Ser Gly Asp Gly Gly Glu Ala Cys
660 665 670

Gly His Pro Glu Pro Arg Gly Gly Pro Ser Thr Pro Gly Lys Cys Thr
139/201

675

680

685

Ser Asp Leu Gln Arg Thr Gln Leu Leu Pro Pro Tyr Pro Leu Asn Gly
 690 695 700

Glu His Thr Gln Ala Gly Thr Ala Met Ser Arg Ala Arg Arg Glu Asp
 705 710 715 720

Leu Pro Ser Leu Arg Lys Glu Glu Ser Cys Leu Leu Gln Arg Ala Thr
 725 730 735

Val Gly Leu Thr Asp Gly Leu Gly Asp Ala Ser Gln Leu Pro Val Ala
 740 745 750

Pro Thr Gly Asp Gln Pro Cys Gln Ala Leu Pro Leu Leu Ser Ser Gln
 755 760 765

Thr Ser Val Ala Glu Arg Leu Val Glu Gln Pro Gln Leu His Pro Asp
 770 775 780

Val Arg Thr Glu Cys Glu Ser Gly Thr Thr Ser Trp Glu Ser Asp Asp
 785 790 795 800

Glu Glu Gln Gly Pro Thr Val Pro Ala Asp Asn Gly Pro Ile Pro Ser
 805 810 815

Leu Val Gly Asp Asp Thr Leu Glu Lys Gly Thr Gly Gln Ala Leu Asp
 820 825 830

Ser His Pro Thr Met Lys Asp Pro Val Asn Val Thr Pro Ser Ser Thr
 835 840 845

Pro Glu Ser Ser Pro Thr Asp Cys Leu Gln Asn Arg Ala Phe Asp Asp
 850 855 860

Glu Leu Gly Leu Gly Gly Ser Cys Pro Pro Met Arg Glu Ser Asp Thr
 865 870 875 880

Arg Gln Glu Asn Leu Lys Thr Lys Ala Leu Val Ser Asn Ser Ser Leu
885 890 895

His Trp Ile Pro Ile Pro Ser Asn Asp Glu Val Val Lys Gln Pro Lys
900 905 910

Pro Glu Ser Arg Glu His Ile Pro Ser Val Glu Pro Gln Val Gly Glu
915 920 925

Glu Trp Glu Lys Ala Ala Pro Thr Pro Pro Ala Leu Pro Gly Asp Leu
930 935 940

Thr Ala Glu Glu Gly Leu Asp Pro Leu Asp Ser Leu Thr Ser Leu Trp
945 950 955 960

Thr Val Pro Ser Arg Gly Gly Ser Asp Ser Asn Gly Ser Tyr Cys Gln
965 970 975

Gln Val Asp Ile Glu Lys Leu Lys Ile Asn Gly Asp Ser Glu Ala Leu
980 985 990

Ser Pro His Gly Glu Ser Thr Asp Thr Ala Ser Asp Phe Glu Gly His
995 1000 1005

Leu Thr Glu Asp Ser Ser Glu Ala Asp Thr Arg Glu Ala Ala Val
1010 1015 1020

Thr Lys Gly Ser Ser Val Asp Lys Asp Glu Lys Pro Asn Trp Asn
1025 1030 1035

Gln Ser Ala Pro Leu Ser Lys Val Asn Gly Asp Met Arg Leu Val
1040 1045 1050

Thr Arg Thr Asp Gly Met Val Ala Pro Gln Ser Trp Val Ser Arg
1055 1060 1065

Val Cys Ala Val Arg Gln Lys Ile Pro Asp Ser Leu Leu Leu Ala
141/201

1070	1075	1080
Ser Thr Glu Tyr Gln Pro Arg Ala Val Cys Leu Ser Met Pro Gly		
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Ser Ser Val Glu Ala Thr Asn Pro Leu Val Met Gln Leu Leu Gln		
1100	1105	1110
Gly Ser Leu Pro Leu Glu Lys Val Leu Pro Pro Ala His Asp Asp		
1115	1120	1125
Ser Met Ser Glu Ser Pro Gln Val Pro Leu Thr Lys Asp Gln Ser		
1130	1135	1140
His Gly Ser Leu Arg Met Gly Ser Leu His Gly Leu Gly Lys Asn		
1145	1150	1155
Ser Gly Met Val Asp Gly Ser Ser Pro Ser Ser Leu Arg Ala Leu		
1160	1165	1170
Lys Glu Pro Leu Leu Pro Asp Ser Cys Glu Thr Gly Thr Gly Leu		
1175	1180	1185
Ala Arg Ile Glu Ala Thr Gln Ala Pro Gly Ala Pro Gln Lys Asn		
1190	1195	1200
Cys Lys Ala Val Pro Ser Phe Asp Ser Leu His Pro Val Thr Asn		
1205	1210	1215
Pro Ile Thr Ser Ser Arg Lys Leu Glu Glu Met Asp Ser Lys Glu		
1220	1225	1230
Gln Phe Ser Ser Phe Ser Cys Glu Asp Gln Lys Glu Val Arg Ala		
1235	1240	1245
Met Ser Gln Asp Ser Asn Ser Asn Ala Ala Pro Gly Lys Ser Pro		
1250	1255	1260

Gly Asp Leu Thr Thr Ser Arg Thr Pro Arg Phe Ser Ser Pro Asn
1265 1270 1275

Val Ile Ser Phe Gly Pro Glu Gln Thr Gly Arg Ala Leu Gly Asp
1280 1285 1290

Gln Ser Asn Val Thr Gly Gln Gly Lys Lys Leu Phe Gly Ser Gly
1295 1300 1305

Asn Val Ala Ala Thr Leu Gln Arg Pro Arg Pro Ala Asp Pro Met
1310 1315 1320

Pro Leu Pro Ala Glu Ile Pro Pro Val Phe Pro Ser Gly Lys Leu
1325 1330 1335

Gly Pro Ser Thr Asn Ser Met Ser Gly Gly Val Gln Thr Pro Arg
1340 1345 1350

Glu Asp Trp Ala Pro Lys Pro His Ala Phe Val Gly Ser Val Lys
1355 1360 1365

Asn Glu Lys Thr Phe Val Gly Gly Pro Leu Lys Ala Asn Ala Glu
1370 1375 1380

Asn Arg Lys Ala Thr Gly His Ser Pro Leu Glu Leu Val Gly His
1385 1390 1395

Leu Glu Gly Met Pro Phe Val Met Asp Leu Pro Phe Trp Lys Leu
1400 1405 1410

Pro Arg Glu Pro Gly Lys Gly Leu Ser Glu Pro Leu Glu Pro Ser
1415 1420 1425

Ser Leu Pro Ser Gln Leu Ser Ile Lys Gln Ala Phe Tyr Gly Lys
1430 1435 1440

Leu Ser Lys Leu Gln Leu Ser Ser Thr Ser Phe Asn Tyr Ser Ser
143/201

1445	1450	1455
Ser Ser Pro Thr Phe Pro Lys Gly Leu Ala Gly Ser Val Val Gln.		
1460	1465	1470
Leu Ser His Lys Ala Asn Phe Gly Ala Ser His Ser Ala Ser Leu		
1475	1480	1485
Ser Leu Gln Met Phe Thr Asp Ser Ser Thr Val Glu Ser Ile Ser		
1490	1495	1500
Leu Gln Cys Ala Cys Ser Leu Lys Ala Met Ile Met Cys Gln Gly		
1505	1510	1515
Cys Gly Ala Phe Cys His Asp Asp Cys Ile Gly Pro Ser Lys Leu		
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Cys Val Leu Cys Leu Val Val Arg		
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gccgcgccgc cgcgcgccgc gcgcacgccg cgcgccgcag ctctgggctt cctcttcgcc	180
cgggtggcgt tgggcccgcg cgggcgctcg ggtgactgca gctgctcagc tcccctccc	240
cgcgccgcgc cgcgcggccg cccgtcgctt cgcacagggc tggatggttg tattgggcag	300
ggtggctcca gg atg tta gga act gtg aag atg gaa ggg cat gaa acc agc	351
Met Leu Gly Thr Val Lys Met Glu Gly His Glu Thr Ser	

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Asp Trp Asn Ser Tyr Tyr Ala Asp Thr Gln Glu Ala Tyr Ser Ser Val			
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ccg gtc agc aac atg aac tca ggc ctg ggc tcc atg aac tcc atg aac			447
Pro Val Ser Asn Met Asn Ser Gly Leu Gly Ser Met Asn Ser Met Asn			
30	35	40	45
acc tac atg acc atg aac acc atg act acg agc ggc aac atg acc ccg			495
Thr Tyr Met Thr Met Asn Thr Met Thr Thr Ser Gly Asn Met Thr Pro			
50	55	60	
gcg tcc ttc aac atg tcc tat gcc aac ccg ggc cta ggg gcc ggc ctg			543
Ala Ser Phe Asn Met Ser Tyr Ala Asn Pro Gly Leu Gly Ala Gly Leu			
65	70	75	
agt ccc ggc gca gta gcc ggc atg ccg ggg ggc tcg gcg ggc gcc atg			591
Ser Pro Gly Ala Val Ala Gly Met Pro Gly Gly Ser Ala Gly Ala Met			
80	85	90	
aac agc atg act gcg gcc ggc gtg acg gcc atg ggt acg gcg ctg agc			639
Asn Ser Met Thr Ala Ala Gly Val Thr Ala Met Gly Thr Ala Leu Ser			
95	100	105	
ccg agc ggc atg ggc gcc atg ggt gcg cag cag gcg gcc tcc atg aat			687
Pro Ser Gly Met Gly Ala Met Gly Ala Gln Gln Ala Ala Ser Met Asn			
110	115	120	125
ggc ctg ggc ccc tac gcg gcc gcc atg aac ccg tgc atg agc ccc atg			735
Gly Leu Gly Pro Tyr Ala Ala Ala Met Asn Pro Cys Met Ser Pro Met			
130	135	140	
gcg tac gcg ccg tcc aac ctg ggc cgc agc cgc gcg ggc ggc ggc ggc			783
Ala Tyr Ala Pro Ser Asn Leu Gly Arg Ser Arg Ala Gly Gly Gly Gly			
145	150	155	
gac gcc aag acg ttc aag cgc agc tac ccg cac gcc aag ccg ccc tac			831
Asp Ala Lys Thr Phe Lys Arg Ser Tyr Pro His Ala Lys Pro Pro Tyr			
160	165	170	
tcg tac atc tcg ctc atc acc atg gcc atc cag cag gcg ccc agc aag			879
Ser Tyr Ile Ser Leu Ile Thr Met Ala Ile Gln Gln Ala Pro Ser Lys			
175	180	185	
atg ctc acg ctg agc gag atc tac cag tgg atc atg gac ctc ttc ccc			927
Met Leu Thr Leu Ser Glu Ile Tyr Gln Trp Ile Met Asp Leu Phe Pro			
190	195	200	205

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ttc gag aac ggc tgc tac ttg cgc cgc cag aag cgc ttc aag tgc gag Phe Glu Asn Gly Cys Tyr Leu Arg Arg Gln Lys Arg Phe Lys Cys Glu 255 260 265	1119
aag cag ccg ggg gcc ggc ggc ggg ggc ggg agc gga agc ggg ggc agc Lys Gln Pro Gly Ala Gly Gly Gly Gly Gly Ser Gly Ser Gly Gly Ser 270 275 280 285	1167
ggc gcc aag ggc ggc cct gag agc cgc aag gac ccc tct ggc gcc tct Gly Ala Lys Gly Gly Pro Glu Ser Arg Lys Asp Pro Ser Gly Ala Ser 290 295 300	1215
aac ccc agc gcc gac tcg ccc ctc cat cgg ggt gtg cac ggg aag acc Asn Pro Ser Ala Asp Ser Pro Leu His Arg Gly Val His Gly Lys Thr 305 310 315	1263
ggc cag cta gag ggc gcg ccg gcc ccc ggg ccc gcc gcc agc ccc cag Gly Gln Leu Glu Gly Ala Pro Ala Pro Gly Pro Ala Ala Ser Pro Gln 320 325 330	1311
act ctg gac cac agt ggg gcg acg gcg aca ggg ggc gcc tcg gag ttg Thr Leu Asp His Ser Gly Ala Thr Ala Thr Gly Gly Ala Ser Glu Leu 335 340 345	1359
aag act cca gcc tcc tca act gcg ccc ccc ata agc tcc ggg ccc ggg Lys Thr Pro Ala Ser Ser Thr Ala Pro Pro Ile Ser Ser Gly Pro Gly 350 355 360 365	1407
gcg ctg gcc tct gtg ccc gcc tct cac ccg gca cac ggc ttg gca ccc Ala Leu Ala Ser Val Pro Ala Ser His Pro Ala His Gly Leu Ala Pro 370 375 380	1455
cac gag tcc cag ctg cac ctg aaa ggg gac ccc cac tac tcc ttc aac His Glu Ser Gln Leu His Leu Lys Gly Asp Pro His Tyr Ser Phe Asn 385 390 395	1503
cac ccg ttc tcc atc aac aac ctc atg tcc tcc tcg gag cag cag cat His Pro Phe Ser Ile Asn Asn Leu Met Ser Ser Ser Glu Gln Gln His 146/201	1551

400	405	410	
aag ctg gac ttc aag gca tac gaa cag gca ctg caa tac tcg cct tac			1599
Lys Leu Asp Phe Lys Ala Tyr Glu Gln Ala Leu Gln Tyr Ser Pro Tyr			
415	420	425	
ggc tct acg ttg ccc gcc agc ctg cct cta ggc agc gcc tcg gtg acc			1647
Gly Ser Thr Leu Pro Ala Ser Leu Pro Leu Gly Ser Ala Ser Val Thr			
430	435	440	445
acc agg agc ccc atc gag ccc tca gcc ctg gag ccg gcg tac tac caa			1695
Thr Arg Ser Pro Ile Glu Pro Ser Ala Leu Glu Pro Ala Tyr Tyr Gln			
	450	455	460
ggt gtg tat tcc aga ccc gtc cta aac act tcc tag ctcccgggac			1741
Gly Val Tyr Ser Arg Pro Val Leu Asn Thr Ser			
	465	470	
tgggggggttt gtctggcata gccatgctgg tagcaagaga gaaaaaatca acagcaaaca			1801
aaaccacaca aaccaaaccg tcaacagcat aataaaatcc caacaactat ttttatttca			1861
tttttcatgc acaacctttc ccccagtgca aaagactggt actttattat tgtattcaaa			1921
attcattgtg tatattacta caaagacaac cccaaaccaa tttttttcct gcgaagttaa			1981
atgatccaca agtgtatata tgaaattctc ctcttctctt gccccctct ctttcttccc			2041
tctttccccct ccagacattc tagtttgtgg agggttatit aaaaaaaca aaaaggaaga			2101
tggtcaagtt tgtaaaatat ttgtttgtgc tttttcccc tccttacctg accccctacg			2161
agtttacagg tctgtggcaa tactcttaac cataagaatt gaaatgggtga agaaacaagt			2221
atacactaga ggctcttaaa agtattgaaa gacaatactg ctggttatata gcaagacata			2281
aacagattat aaacatcaga gccatttgct tctcagttta catttctgat acatgcagat			2341
agcagatgtc tttaaataaa atacatgtat attgtgtatg gacttaatta tgcacatgct			2401
cagatgtgta gacatcctcc gtatatttac ataacatata gaggtaatag ataggtgata			2461
tacatgatac attctcaaga gttgcttgac cgaaagttac aaggacccca acccctttgt			2521
cctctctacc cacagatggc cctgggaatc aattcctcag gaattgccct caagaactct			2581
gcttcttgct ttgcagagtg ccatgggtcat gtcattctga ggtaacataa cacataaaat			2641
tagtttctat gagtgtatac catttaaaga attttttttt cagtaaaagg gaatattaca			2701

atgttggagg agagataagt tatagggagc tggatttcaa aacgtgggtcc aagattcaaa 2761
 aatcctattg atagtggcca ttttaatcat tgccatcgtg tgcttgtttc atccagtgtt 2821
 atgcactttc cacagttgga catgggtgtta gtatagccag acgggtttca ttattatttc 2881
 tctttgcttt ctcaatgtta atttattgca tggttttattc tttttcttta cagctgaaat 2941
 tgctttaaat gatgggttaaa attacaaatt aaattgttaa tttttatcaa tgtgattgta 3001
 attaaaaata ttttgattta aataacaaaa ataataccag attttaagcc gtggaaaatg 3061
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 aaa 3124

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 <213> Homo sapiens

<400> 50

Met Leu Gly Thr Val Lys Met Glu Gly His Glu Thr Ser Asp Trp Asn
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Ser Tyr Tyr Ala Asp Thr Gln Glu Ala Tyr Ser Ser Val Pro Val Ser
 20 25 30

Asn Met Asn Ser Gly Leu Gly Ser Met Asn Ser Met Asn Thr Tyr Met
 35 40 45

Thr Met Asn Thr Met Thr Thr Ser Gly Asn Met Thr Pro Ala Ser Phe
 50 55 60

Asn Met Ser Tyr Ala Asn Pro Gly Leu Gly Ala Gly Leu Ser Pro Gly
 65 70 75 80

Ala Val Ala Gly Met Pro Gly Gly Ser Ala Gly Ala Met Asn Ser Met
 85 90 95

Thr Ala Ala Gly Val Thr Ala Met Gly Thr Ala Leu Ser Pro Ser Gly
 100 105 110

Met Gly Ala Met Gly Ala Gln Gln Ala Ala Ser Met Asn Gly Leu Gly
115 120 125

Pro Tyr Ala Ala Ala Met Asn Pro Cys Met Ser Pro Met Ala Tyr Ala
130 135 140

Pro Ser Asn Leu Gly Arg Ser Arg Ala Gly Gly Gly Gly Asp Ala Lys
145 150 155 160

Thr Phe Lys Arg Ser Tyr Pro His Ala Lys Pro Pro Tyr Ser Tyr Ile
165 170 175

Ser Leu Ile Thr Met Ala Ile Gln Gln Ala Pro Ser Lys Met Leu Thr
180 185 190

Leu Ser Glu Ile Tyr Gln Trp Ile Met Asp Leu Phe Pro Tyr Tyr Arg
195 200 205

Gln Asn Gln Gln Arg Trp Gln Asn Ser Ile Arg His Ser Leu Ser Phe
210 215 220

Asn Asp Cys Phe Val Lys Val Ala Arg Ser Pro Asp Lys Pro Gly Lys
225 230 235 240

Gly Ser Tyr Trp Thr Leu His Pro Asp Ser Gly Asn Met Phe Glu Asn
245 250 255

Gly Cys Tyr Leu Arg Arg Gln Lys Arg Phe Lys Cys Glu Lys Gln Pro
260 265 270

Gly Ala Gly Gly Gly Gly Gly Ser Gly Ser Gly Gly Ser Gly Ala Lys
275 280 285

Gly Gly Pro Glu Ser Arg Lys Asp Pro Ser Gly Ala Ser Asn Pro Ser
290 295 300

Ala Asp Ser Pro Leu His Arg Gly Val His Gly Lys Thr Gly Gln Leu
305 310 315 320

Glu Gly Ala Pro Ala Pro Gly Pro Ala Ala Ser Pro Gln Thr Leu Asp
325 330 335

His Ser Gly Ala Thr Ala Thr Gly Gly Ala Ser Glu Leu Lys Thr Pro
340 345 350

Ala Ser Ser Thr Ala Pro Pro Ile Ser Ser Gly Pro Gly Ala Leu Ala
355 360 365

Ser Val Pro Ala Ser His Pro Ala His Gly Leu Ala Pro His Glu Ser
370 375 380

Gln Leu His Leu Lys Gly Asp Pro His Tyr Ser Phe Asn His Pro Phe
385 390 395 400

Ser Ile Asn Asn Leu Met Ser Ser Ser Glu Gln Gln His Lys Leu Asp
405 410 415

Phe Lys Ala Tyr Glu Gln Ala Leu Gln Tyr Ser Pro Tyr Gly Ser Thr
420 425 430

Leu Pro Ala Ser Leu Pro Leu Gly Ser Ala Ser Val Thr Thr Arg Ser
435 440 445

Pro Ile Glu Pro Ser Ala Leu Glu Pro Ala Tyr Tyr Gln Gly Val Tyr
450 455 460

Ser Arg Pro Val Leu Asn Thr Ser
465 470

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 caggccttcg tggagcactg gaagggcac acgcactact acatcgagag cacagatgaa 180
 agcaccctcg ccaagaagac agacattccc tggcggctga agcagatgct ggatatcctg 240
 gtgtatgaag agcagcagca ggcggccgcg ggtgaggcag ggccctgcct ggagtacctg 300
 ctgcagcaca agatcctgga gactctctgc acgctgggca aggccgagta cccccaggc 360
 atgcggcagc aggtgttcca gttcttcagc aaggttcttg cgcagggtgca gcaccctctg 420
 ctgcattacc tcagcgtcca caggcctgtg cagaaactcc tccgacttgg tgggactgct 480
 tccggatccg ttacagaaaa ggaggaggtg cagttcacca ccgtcctctg ctccaagatc 540
 cagcaggacc cagagctgct cgcctacatc ctggaaggta aaaagattgt aggtaggaag 600
 aaagcatgcg gagaaccac tgccctgcct aaggacacaa ccagccacgg ggacaaggac 660
 tgctcccacg atggtgctcc tgccaggccc cagctggacg gggagtcctg tggggcccag 720
 gccttgaaca gccacatgcc tgctgagacc gaggagctgg acggtgggac cacagagagc 780
 aacctgatta cctccctgct tgggctgtgc cagagcaaga agagtcgggt ggccttgaag 840
 gccagagaga acctgctgct cctgggtgagc atggcctccc cagcagctgc cacctacctg 900
 gtacagagca gcgcctgctg ccctgcgac gtccggcact ttgccagttg taccggctcc 959
 atg cct gtc ttc ctg gac ccc gca gac att gcc acc tta gag ggc atc 1007
 Met Pro Val Phe Leu Asp Pro Ala Asp Ile Ala Thr Leu Glu Gly Ile
 1 5 10 15
 agc tgg agg tta ccc agt gcc ccg tct gat gag gct tcc ttc cct ggc 1055
 Ser Trp Arg Leu Pro Ser Ala Pro Ser Asp Glu Ala Ser Phe Pro Gly
 20 25 30
 aag gag gcc ttg gct gcc ttc ttg ggc tgg ttt gat tac tgc gac cac 1103
 Lys Glu Ala Leu Ala Ala Phe Leu Gly Trp Phe Asp Tyr Cys Asp His
 35 40 45
 ctc atc aca gag gca cac acg gtg gtt gcg gac gcc ttg gcg aag gct 1151

Leu	Ile	Thr	Glu	Ala	His	Thr	Val	Val	Ala	Asp	Ala	Leu	Ala	Lys	Ala		
50						55					60						
gtg	gct	gag	aac	ttc	ttc	gtg	gag	acc	ctg	cag	ccc	cag	ctc	ctg	cac		1199
Val	Ala	Glu	Asn	Phe	Phe	Val	Glu	Thr	Leu	Gln	Pro	Gln	Leu	Leu	His		
65					70					75					80		
gtg	tcc	gag	cag	agc	atc	ttg	acc	tcc	acc	gcc	ctc	ctc	aca	gcc	atg		1247
Val	Ser	Glu	Gln	Ser	Ile	Leu	Thr	Ser	Thr	Ala	Leu	Leu	Thr	Ala	Met		
				85					90					95			
ctg	cgc	cag	ctt	cgc	tcc	cct	gcg	ctg	ctg	cgg	gag	gcc	gtg	gct	ttc		1295
Leu	Arg	Gln	Leu	Arg	Ser	Pro	Ala	Leu	Leu	Arg	Glu	Ala	Val	Ala	Phe		
			100					105					110				
ctc	ctg	ggc	aca	gac	cgg	cag	cct	gaa	gcc	ccc	ggg	gac	aac	ccc	cac		1343
Leu	Leu	Gly	Thr	Asp	Arg	Gln	Pro	Glu	Ala	Pro	Gly	Asp	Asn	Pro	His		
		115					120					125					
acc	ctg	tat	gct	cat	ctc	atc	ggg	cat	tgt	gac	cac	ctc	tct	gat	gag		1391
Thr	Leu	Tyr	Ala	His	Leu	Ile	Gly	His	Cys	Asp	His	Leu	Ser	Asp	Glu		
	130					135					140						
atc	agc	atc	acc	aca	ctc	cgg	ctg	ttt	gag	gag	ctg	ctg	cag	aag	ccc		1439
Ile	Ser	Ile	Thr	Thr	Leu	Arg	Leu	Phe	Glu	Glu	Leu	Leu	Gln	Lys	Pro		
145					150					155					160		
cac	gag	ggg	atc	atc	cac	agc	ctg	gtc	ctg	cgc	aac	ctt	gag	ggc	cgc		1487
His	Glu	Gly	Ile	Ile	His	Ser	Leu	Val	Leu	Arg	Asn	Leu	Glu	Gly	Arg		
				165					170						175		
cct	tac	gtg	gcc	tgg	ggc	tca	cca	gag	cct	gag	agc	tat	gag	gac	acc		1535
Pro	Tyr	Val	Ala	Trp	Gly	Ser	Pro	Glu	Pro	Glu	Ser	Tyr	Glu	Asp	Thr		
			180					185					190				
cta	gac	ctg	gag	gaa	gac	ccc	tac	ttc	acc	gac	agc	ttc	ctg	gat	tcc		1583
Leu	Asp	Leu	Glu	Glu	Asp	Pro	Tyr	Phe	Thr	Asp	Ser	Phe	Leu	Asp	Ser		
		195					200					205					
ggc	ttt	caa	act	ccc	gca	aag	cct	cgc	cta	gct	cct	gct	acc	agt	tac		1631
Gly	Phe	Gln	Thr	Pro	Ala	Lys	Pro	Arg	Leu	Ala	Pro	Ala	Thr	Ser	Tyr		
	210					215					220						
gat	ggc	aaa	aca	gca	gtg	acc	gag	atc	gtc	aac	agt	ttc	ctg	tgc	ctg		1679
Asp	Gly	Lys	Thr	Ala	Val	Thr	Glu	Ile	Val	Asn	Ser	Phe	Leu	Cys	Leu		
225					230					235					240		
gtc	ccc	gag	gaa	gcc	aag	acc	tct	gcc	ttc	ctg	gag	gag	aca	ggc	tat		1727
Val	Pro	Glu	Glu	Ala	Lys	Thr	Ser	Ala	Phe	Leu	Glu	Glu	Thr	Gly	Tyr		
				245					250					255			

gac aca tac gtc cac gat gct tat ggc ctg ttc cag gag tgc agc tcc Asp Thr Tyr Val His Asp Ala Tyr Gly Leu Phe Gln Glu Cys Ser Ser	1775
260 265 270	
cgc gtc gcc tcc tgg ggc tgg cct ctg acc ccc aca cct ttg gac ccc Arg Val Ala Ser Trp Gly Trp Pro Leu Thr Pro Thr Pro Leu Asp Pro	1823
275 280 285	
cat gag ccc gag cga cct ttc ttc gag ggc cac ttc ctc cga gtg ctg His Glu Pro Glu Arg Pro Phe Phe Glu Gly His Phe Leu Arg Val Leu	1871
290 295 300	
ttt gac cgc atg tcc cgg att ctg gat cag cca tac agc ctg aac ctg Phe Asp Arg Met Ser Arg Ile Leu Asp Gln Pro Tyr Ser Leu Asn Leu	1919
305 310 315 320	
cag gtg acc tcg gtc ctg tcc cgg ctt gcc ctc ttc ccc cac ccc cat Gln Val Thr Ser Val Leu Ser Arg Leu Ala Leu Phe Pro His Pro His	1967
325 330 335	
att cat gag tac ctg ctg gat ccg tac atc agc ctg gcc ccc ggc tgc Ile His Glu Tyr Leu Leu Asp Pro Tyr Ile Ser Leu Ala Pro Gly Cys	2015
340 345 350	
agg agc cta ttc tcc gtg ttg gtg agg gtg atc ggg gac ttg atg cag Arg Ser Leu Phe Ser Val Leu Val Arg Val Ile Gly Asp Leu Met Gln	2063
355 360 365	
aga atc cag agg gta ccc cag ttc cca ggc aag ctg ctc ctg gtg cgc Arg Ile Gln Arg Val Pro Gln Phe Pro Gly Lys Leu Leu Leu Val Arg	2111
370 375 380	
aag cag ttg acg ggc cag gct cct ggg gag cag ctg gac cac cag acc Lys Gln Leu Thr Gly Gln Ala Pro Gly Glu Gln Leu Asp His Gln Thr	2159
385 390 395 400	
ctc ctc cag ggc gtg gtg gtg ctg gag gag ttc tgc aag gag ctg gct Leu Leu Gln Gly Val Val Val Leu Glu Glu Phe Cys Lys Glu Leu Ala	2207
405 410 415	
gcc att gcc ttc gtc aag ttt ccc cca cat gat cct cgc cag aac gtc Ala Ile Ala Phe Val Lys Phe Pro Pro His Asp Pro Arg Gln Asn Val	2255
420 425 430	
tcc cca gcc ccg gaa ggg cag gtc tga gccagcacca gggcgggtggg Ser Pro Ala Pro Glu Gly Gln Val	2302
435 440	
agactcctgt ccacacctct gccccagagc tgcctcctgc ctggcactgc cgccacactc	2362

ccctcctggg atggggcttc tgctcccggg ctactcaag gagactgcgg catgttgacc	2422
acaccagact gggtttcagg gaatgggcat gccaggtgcc aaggagccaa acagatggct	2482
ttccaggcag caaggtcctt ggggccttct tggaggagct tgggtgacag ccaggtgagc	2542
accagaccc cagaccctca tgtgctgtgt gcctggcccc ttctgtactg gccatttgtg	2602
gccagggcca agcctgtgac tcaactccag gggcaagatg gggagtgagc tgatggctcc	2662
gagactggtc aggagcccag gccagtgaga tggggcctgg agccttgtct gtgtcacatt	2722
aggtaccatg ggagctgctg agacctgaca ttttgtcccc tgcctacatg gcttggccca	2782
tggagaagga gcagtgaatg ggategtcgg ggaagcccct ctccctgctc tgctcccctg	2842
gaaactgttg caaaactccc agccgcctca tggcaaatgc ccaaagcatg ttccgcaccc	2902
aggcgggggc ccctgctaata gagaaccttg gtgcagctgc agccaggagg ggagcgggcc	2962
caggagccag gctcaggtcc agctgggttc tctctggcgc cttctgaacc cgtctcagca	3022
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tgcccagggc ccagtgttct tgatagaaga cccttctggg gagccaggga gctcagggga	3142
cagataaggg aaggacgcc cctgactcca ggcccctgag cctggcggga agtggctgcg	3202
gcccaggcag ccagtcctgg tgggtgttct cctgcatgcc ctccgtggct gggctgccac	3262
cccacccggc ccgaatctgt cttgacctgc aggaatacac gggcggcgcc aggcattacc	3322
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gggaggacct cgccgctctg aagagcaccg tgcacatgtg ggtgcacaaa cgtgggtgtt	3562
ggtgtggacg gggcgcagat ctccgtggat gaactgcgtc tggactctta gattcataaa	3622
atattcgagg gtttgggagt cacagaccct cccctctcct cagtgcactt tggcatttgc	3682
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	3780

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<211> 440
<212> PRT
<213> Homo sapiens

<400> 52

Met Pro Val Phe Leu Asp Pro Ala Asp Ile Ala Thr Leu Glu Gly Ile
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Ser Trp Arg Leu Pro Ser Ala Pro Ser Asp Glu Ala Ser Phe Pro Gly
20 25 30

Lys Glu Ala Leu Ala Ala Phe Leu Gly Trp Phe Asp Tyr Cys Asp His
35 40 45

Leu Ile Thr Glu Ala His Thr Val Val Ala Asp Ala Leu Ala Lys Ala
50 55 60

Val Ala Glu Asn Phe Phe Val Glu Thr Leu Gln Pro Gln Leu Leu His
65 70 75 80

Val Ser Glu Gln Ser Ile Leu Thr Ser Thr Ala Leu Leu Thr Ala Met
85 90 95

Leu Arg Gln Leu Arg Ser Pro Ala Leu Leu Arg Glu Ala Val Ala Phe
100 105 110

Leu Leu Gly Thr Asp Arg Gln Pro Glu Ala Pro Gly Asp Asn Pro His
115 120 125

Thr Leu Tyr Ala His Leu Ile Gly His Cys Asp His Leu Ser Asp Glu
130 135 140

Ile Ser Ile Thr Thr Leu Arg Leu Phe Glu Glu Leu Leu Gln Lys Pro
145 150 155 160

His Glu Gly Ile Ile His Ser Leu Val Leu Arg Asn Leu Glu Gly Arg
165 170 175

Pro Tyr Val Ala Trp Gly Ser Pro Glu Pro Glu Ser Tyr Glu Asp Thr
180 185 190

Leu Asp Leu Glu Glu Asp Pro Tyr Phe Thr Asp Ser Phe Leu Asp Ser
195 200 205

Gly Phe Gln Thr Pro Ala Lys Pro Arg Leu Ala Pro Ala Thr Ser Tyr
210 215 220

Asp Gly Lys Thr Ala Val Thr Glu Ile Val Asn Ser Phe Leu Cys Leu
225 230 235 240

Val Pro Glu Glu Ala Lys Thr Ser Ala Phe Leu Glu Glu Thr Gly Tyr
245 250 255

Asp Thr Tyr Val His Asp Ala Tyr Gly Leu Phe Gln Glu Cys Ser Ser
260 265 270

Arg Val Ala Ser Trp Gly Trp Pro Leu Thr Pro Thr Pro Leu Asp Pro
275 280 285

His Glu Pro Glu Arg Pro Phe Phe Glu Gly His Phe Leu Arg Val Leu
290 295 300

Phe Asp Arg Met Ser Arg Ile Leu Asp Gln Pro Tyr Ser Leu Asn Leu
305 310 315 320

Gln Val Thr Ser Val Leu Ser Arg Leu Ala Leu Phe Pro His Pro His
325 330 335

Ile His Glu Tyr Leu Leu Asp Pro Tyr Ile Ser Leu Ala Pro Gly Cys
340 345 350

Arg Ser Leu Phe Ser Val Leu Val Arg Val Ile Gly Asp Leu Met Gln
355 360 365

Arg Ile Gln Arg Val Pro Gln Phe Pro Gly Lys Leu Leu Leu Val Arg
156/201

370

375

380

Lys Gln Leu Thr Gly Gln Ala Pro Gly Glu Gln Leu Asp His Gln Thr
 385 390 395 400

Leu Leu Gln Gly Val Val Val Leu Glu Glu Phe Cys Lys Glu Leu Ala
 405 410 415

Ala Ile Ala Phe Val Lys Phe Pro Pro His Asp Pro Arg Gln Asn Val
 420 425 430

Ser Pro Ala Pro Glu Gly Gln Val
 435 440

<210> 53
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 <222> (68).. (895)
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 Met Gln Asn Asn Glu Ile Ile Lys Pro Ala Lys Tyr Phe Ser
 1 5 10
 gaa ttg gaa aag agc atc ctg ctg gct tta gta gaa aag tat aaa tat 157
 Glu Leu Glu Lys Ser Ile Leu Leu Ala Leu Val Glu Lys Tyr Lys Tyr
 15 20 25 30
 gtg ctg gaa tgt aag aaa agt gat gcg cga act att gcc ctt aag cag 205
 Val Leu Glu Cys Lys Lys Ser Asp Ala Arg Thr Ile Ala Leu Lys Gln
 35 40 45
 cgt acc tgg cag gcg ctg gcc cac gaa tac aac tct cag ccc agc gtg 253
 Arg Thr Trp Gln Ala Leu Ala His Glu Tyr Asn Ser Gln Pro Ser Val
 50 55 60
 tcc ctg cgg gat ttc aaa cag ctg aag aag tgc tgg gag aac atc aag 301
 Ser Leu Arg Asp Phe Lys Gln Leu Lys Lys Cys Trp Glu Asn Ile Lys
 157/201

65	70	75	
gct cgg acc aaa aaa att atg gcc cat gaa agg aga gag aaa gtg aaa			349
Ala Arg Thr Lys Lys Ile Met Ala His Glu Arg Arg Glu Lys Val Lys			
80	85	90	
cgg agc gtc agc cct ctc ctg agt acc cac gtc cta ggg aag gag aag			397
Arg Ser Val Ser Pro Leu Leu Ser Thr His Val Leu Gly Lys Glu Lys			
95	100	105	110
atc gcc agc atg ctg ccg gag cag ctc tac ttc ctg cag agc ccc ccg			445
Ile Ala Ser Met Leu Pro Glu Gln Leu Tyr Phe Leu Gln Ser Pro Pro			
115	120	125	
gag gag gag ccc gaa tac cac ccc gac gcc tca gcc caa gaa tca ttt			493
Glu Glu Glu Pro Glu Tyr His Pro Asp Ala Ser Ala Gln Glu Ser Phe			
130	135	140	
gct gtt tca aat aga gaa ctg tgc gat gat gag aaa gag ttc ata cat			541
Ala Val Ser Asn Arg Glu Leu Cys Asp Asp Glu Lys Glu Phe Ile His			
145	150	155	
ttt cca gta tgt gag ggg acc tct caa cct gaa ccc tcg tgt tca gct			589
Phe Pro Val Cys Glu Gly Thr Ser Gln Pro Glu Pro Ser Cys Ser Ala			
160	165	170	
gtc aga ata aca gcc aat aaa aac tac agg agc aaa acc tct cag gaa			637
Val Arg Ile Thr Ala Asn Lys Asn Tyr Arg Ser Lys Thr Ser Gln Glu			
175	180	185	190
ggt gct tta aaa aag atg cat gag gaa gaa cac cat caa caa atg tcc			685
Gly Ala Leu Lys Lys Met His Glu Glu Glu His His Gln Gln Met Ser			
195	200	205	
atc tta caa ctg caa ctg ata caa atg aat gag gtg cat gtg gcc aaa			733
Ile Leu Gln Leu Gln Leu Ile Gln Met Asn Glu Val His Val Ala Lys			
210	215	220	
atc cag cag ata gag cga gag tgt gag atg gca gag gag gaa cac agg			781
Ile Gln Gln Ile Glu Arg Glu Cys Glu Met Ala Glu Glu Glu His Arg			
225	230	235	
ata aaa atg gaa gtt ctc aat aaa aag aag atg tat tgg gaa aga aaa			829
Ile Lys Met Glu Val Leu Asn Lys Lys Lys Met Tyr Trp Glu Arg Lys			
240	245	250	
cta caa act ttt acc aag gaa tgg cct gtt tcc tca ttt aac cgg ccc			877
Leu Gln Thr Phe Thr Lys Glu Trp Pro Val Ser Ser Phe Asn Arg Pro			
255	260	265	270

ttt ccc aat tcg ccc taa gactttgggg gtggctctct tgtaattaat 925
Phe Pro Asn Ser Pro
275

ctgtgttggc aaagaatgtc tggaacatgg acttggcggc cagtaacctg taacagagct 985
acaactagga aaattagagt ggtagtagtc acttatttaa gaattcattc aggtaaacag 1045
ctgcaccctc tgtaccctt aagtggcaaa gaagctgtta tagtcttctg aaaattatca 1105
ctatgagtgc tataattctg aatataatgt ctcttaatta gaattcatac aagaaaaaaaa 1165
aaaaaaaaaa 1175

<210> 54
<211> 275
<212> PRT
<213> Homo sapiens

<400> 54

Met Gln Asn Asn Glu Ile Ile Lys Pro Ala Lys Tyr Phe Ser Glu Leu
1 5 10 15

Glu Lys Ser Ile Leu Leu Ala Leu Val Glu Lys Tyr Lys Tyr Val Leu
20 25 30

Glu Cys Lys Lys Ser Asp Ala Arg Thr Ile Ala Leu Lys Gln Arg Thr
35 40 45

Trp Gln Ala Leu Ala His Glu Tyr Asn Ser Gln Pro Ser Val Ser Leu
50 55 60

Arg Asp Phe Lys Gln Leu Lys Lys Cys Trp Glu Asn Ile Lys Ala Arg
65 70 75 80

Thr Lys Lys Ile Met Ala His Glu Arg Arg Glu Lys Val Lys Arg Ser
85 90 95

Val Ser Pro Leu Leu Ser Thr His Val Leu Gly Lys Glu Lys Ile Ala
100 105 110

Ser Met Leu Pro Glu Gln Leu Tyr Phe Leu Gln Ser Pro Pro Glu Glu
115 120 125

Glu Pro Glu Tyr His Pro Asp Ala Ser Ala Gln Glu Ser Phe Ala Val
130 135 140

Ser Asn Arg Glu Leu Cys Asp Asp Glu Lys Glu Phe Ile His Phe Pro
145 150 155 160

Val Cys Glu Gly Thr Ser Gln Pro Glu Pro Ser Cys Ser Ala Val Arg
165 170 175

Ile Thr Ala Asn Lys Asn Tyr Arg Ser Lys Thr Ser Gln Glu Gly Ala
180 185 190

Leu Lys Lys Met His Glu Glu Glu His His Gln Gln Met Ser Ile Leu
195 200 205

Gln Leu Gln Leu Ile Gln Met Asn Glu Val His Val Ala Lys Ile Gln
210 215 220

Gln Ile Glu Arg Glu Cys Glu Met Ala Glu Glu Glu His Arg Ile Lys
225 230 235 240

Met Glu Val Leu Asn Lys Lys Lys Met Tyr Trp Glu Arg Lys Leu Gln
245 250 255

Thr Phe Thr Lys Glu Trp Pro Val Ser Ser Phe Asn Arg Pro Phe Pro
260 265 270

Asn Ser Pro
275

<210> 55
<211> 1988
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> (12)..(1805)
<223>

<400> 55

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Met Ala Ala Val Gln Ala Ala Glu Val Lys Val Asp Gly	
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agc gag ccg aaa ctg agc aag aat gag ctg aag aga cgc ctg aaa gct	98
Ser Glu Pro Lys Leu Ser Lys Asn Glu Leu Lys Arg Arg Leu Lys Ala	
15 20 25	
gag aag aaa gta gca gag aag gag gcc aaa cag aag gag ctc agt gag	146
Glu Lys Lys Val Ala Glu Lys Glu Ala Lys Gln Lys Glu Leu Ser Glu	
30 35 40 45	
aaa cag cta agc caa gcc act gct gct gcc acc aac cac acc act gat	194
Lys Gln Leu Ser Gln Ala Thr Ala Ala Thr Asn His Thr Thr Asp	
50 55 60	
aat ggt gtg ggt cct gag gaa gag agc gtg gac cca aat caa tac tac	242
Asn Gly Val Gly Pro Glu Glu Glu Ser Val Asp Pro Asn Gln Tyr Tyr	
65 70 75	
aaa atc cgc agt caa gca att cat cag ctg aag gtc aat ggg gaa gac	290
Lys Ile Arg Ser Gln Ala Ile His Gln Leu Lys Val Asn Gly Glu Asp	
80 85 90	
cca tac cca cac aag ttc cat gta gac atc tca ctc act gac ttc atc	338
Pro Tyr Pro His Lys Phe His Val Asp Ile Ser Leu Thr Asp Phe Ile	
95 100 105	
caa aaa tat agt cac ctg cag cct ggg gat cac ctg act gac atc acc	386
Gln Lys Tyr Ser His Leu Gln Pro Gly Asp His Leu Thr Asp Ile Thr	
110 115 120 125	
tta aag gtg gca ggt agg atc cat gcc aaa aga gct tct ggg gga aag	434
Leu Lys Val Ala Gly Arg Ile His Ala Lys Arg Ala Ser Gly Gly Lys	
130 135 140	
ctc atc ttc tat gat ctt cga gga gag ggg gtg aag ttg caa gtc atg	482
Leu Ile Phe Tyr Asp Leu Arg Gly Glu Gly Val Lys Leu Gln Val Met	
145 150 155	
gcc aat tcc aga aat tat aaa tca gaa gaa gaa ttt att cat att aat	530
Ala Asn Ser Arg Asn Tyr Lys Ser Glu Glu Glu Phe Ile His Ile Asn	
160 165 170	
aac aaa ctg cgt cgg gga gac ata att gga gtt cag ggg aat cct ggt	578

Asn Lys Leu Arg Arg Gly Asp Ile Ile Gly Val Gln Gly Asn Pro Gly	
175 180 185	
aaa acc aag aag ggt gag ctg agc atc att ccg tat gag atc aca ctg	626
Lys Thr Lys Lys Gly Glu Leu Ser Ile Ile Pro Tyr Glu Ile Thr Leu	
190 195 200 205	
ctg tct ccc tgt ttg cat atg tta cct cat ctt cac ttt ggc ctc aaa	674
Leu Ser Pro Cys Leu His Met Leu Pro His Leu His Phe Gly Leu Lys	
210 215 220	
gac aag gaa aca agg tat cgc cag aga tac ttg gac ttg atc ctg aat	722
Asp Lys Glu Thr Arg Tyr Arg Gln Arg Tyr Leu Asp Leu Ile Leu Asn	
225 230 235	
gac ttt gtg agg cag aaa ttt atc atc cgc tct aag atc atc aca tat	770
Asp Phe Val Arg Gln Lys Phe Ile Ile Arg Ser Lys Ile Ile Thr Tyr	
240 245 250	
ata aga agt ttc tta gat gag ctg gga ttc cta gag att gaa act ccc	818
Ile Arg Ser Phe Leu Asp Glu Leu Gly Phe Leu Glu Ile Glu Thr Pro	
255 260 265	
atg atg aac atc atc cca ggg gga gcc gtg gcc aag cct ttc atc act	866
Met Met Asn Ile Ile Pro Gly Gly Ala Val Ala Lys Pro Phe Ile Thr	
270 275 280 285	
tat cac aac gag ctg gac atg aac tta tat atg aga att gct cca gaa	914
Tyr His Asn Glu Leu Asp Met Asn Leu Tyr Met Arg Ile Ala Pro Glu	
290 295 300	
ctc tat cat aag atg ctt gtg gtt ggt ggc atc gac cgg gtt tat gaa	962
Leu Tyr His Lys Met Leu Val Val Gly Gly Ile Asp Arg Val Tyr Glu	
305 310 315	
att gga cgc cag ttc cgg aat gag ggg att gat ttg acg cac aat cct	1010
Ile Gly Arg Gln Phe Arg Asn Glu Gly Ile Asp Leu Thr His Asn Pro	
320 325 330	
gag ttc acc acc tgt gag ttc tac atg gcc tat gca gac tat cac gat	1058
Glu Phe Thr Thr Cys Glu Phe Tyr Met Ala Tyr Ala Asp Tyr His Asp	
335 340 345	
ctc atg gaa atc acg gag aag atg gtt tca ggg atg gtg aag cat att	1106
Leu Met Glu Ile Thr Glu Lys Met Val Ser Gly Met Val Lys His Ile	
350 355 360 365	
aca ggc agt tac aag gtc acc tac cac cca gat ggc cca gag ggc caa	1154
Thr Gly Ser Tyr Lys Val Thr Tyr His Pro Asp Gly Pro Glu Gly Gln	
370 375 380	

gcc tac gat gtt gac ttc acc cca ccc ttc cgg cga atc aac atg gta	1202
Ala Tyr Asp Val Asp Phe Thr Pro Pro Phe Arg Arg Ile Asn Met Val	
385 390 395	
gaa gag ctt gag aaa gcc ctg ggg atg aag ctg cca gaa acg aac ctc	1250
Glu Glu Leu Glu Lys Ala Leu Gly Met Lys Leu Pro Glu Thr Asn Leu	
400 405 410	
ttt gaa act gaa gaa act cgc aaa att ctt gat gat atc tgt gtg gca	1298
Phe Glu Thr Glu Glu Thr Arg Lys Ile Leu Asp Asp Ile Cys Val Ala	
415 420 425	
aaa gct gtt gaa tgc cct cca cct cgg acc aca gcc agg ctc ctt gac	1346
Lys Ala Val Glu Cys Pro Pro Pro Arg Thr Thr Ala Arg Leu Leu Asp	
430 435 440 445	
aag ctt gtt ggg gag ttc ctg gaa gtg act tgc atc aat cct aca ttc	1394
Lys Leu Val Gly Glu Phe Leu Glu Val Thr Cys Ile Asn Pro Thr Phe	
450 455 460	
atc tgt gat cac cca cag ata atg agc cct ttg gct aaa tgg cac cgc	1442
Ile Cys Asp His Pro Gln Ile Met Ser Pro Leu Ala Lys Trp His Arg	
465 470 475	
tct aaa gag ggt ctg act gag cgc ttt gag ctg ttt gtc atg aag aaa	1490
Ser Lys Glu Gly Leu Thr Glu Arg Phe Glu Leu Phe Val Met Lys Lys	
480 485 490	
gag ata tgc aat gcg tat act gag ctg aat gat ccc atg cgg cag cgg	1538
Glu Ile Cys Asn Ala Tyr Thr Glu Leu Asn Asp Pro Met Arg Gln Arg	
495 500 505	
cag ctt ttt gaa gaa cag gcc aag gcc aag gct gca ggt gat gat gag	1586
Gln Leu Phe Glu Glu Gln Ala Lys Ala Lys Ala Ala Gly Asp Asp Glu	
510 515 520 525	
gcc atg ttc ata gat gaa aac ttc tgt act gcc ctg gaa tat ggg ctg	1634
Ala Met Phe Ile Asp Glu Asn Phe Cys Thr Ala Leu Glu Tyr Gly Leu	
530 535 540	
ccc ccc aca gct ggc tgg ggc atg ggc att gat cga gtc gcc atg ttt	1682
Pro Pro Thr Ala Gly Trp Gly Met Gly Ile Asp Arg Val Ala Met Phe	
545 550 555	
ctc acg gac tcc aac aac atc aag gaa gta ctt ctg ttt cct gcc atg	1730
Leu Thr Asp Ser Asn Asn Ile Lys Glu Val Leu Leu Phe Pro Ala Met	
560 565 570	
aaa ccc gaa gac aag aag gag aat gta gca acc act gat aca ctg gaa	1778
163/201	

Lys Pro Glu Asp Lys Lys Glu Asn Val Ala Thr Thr Asp Thr Leu Glu
575 580 585

agc aca aca gtt ggc act tct gtc tag aaaataataa ttgcaagttg 1825
Ser Thr Thr Val Gly Thr Ser Val
590 595

tataactcag gcgtctttgc atttctgcga aagatcaagg tctgcaaggg aattcttgtg 1885

tgctgctttc catttgacac cgcagttctg ttcagccatc agaagagaga caaggaatta 1945

aaaatttctt tttaatcctg ttaccaaaaa aaaaaaaaaa aaa 1988

<210> 56

<211> 597

<212> PRT

<213> Homo sapiens

<400> 56

Met Ala Ala Val Gln Ala Ala Glu Val Lys Val Asp Gly Ser Glu Pro
1 5 10 15

Lys Leu Ser Lys Asn Glu Leu Lys Arg Arg Leu Lys Ala Glu Lys Lys
20 25 30

Val Ala Glu Lys Glu Ala Lys Gln Lys Glu Leu Ser Glu Lys Gln Leu
35 40 45

Ser Gln Ala Thr Ala Ala Ala Thr Asn His Thr Thr Asp Asn Gly Val
50 55 60

Gly Pro Glu Glu Glu Ser Val Asp Pro Asn Gln Tyr Tyr Lys Ile Arg
65 70 75 80

Ser Gln Ala Ile His Gln Leu Lys Val Asn Gly Glu Asp Pro Tyr Pro
85 90 95

His Lys Phe His Val Asp Ile Ser Leu Thr Asp Phe Ile Gln Lys Tyr
100 105 110

Ser His Leu Gln Pro Gly Asp His Leu Thr Asp Ile Thr Leu Lys Val
164/201

115

120

125

Ala Gly Arg Ile His Ala Lys Arg Ala Ser Gly Gly Lys Leu Ile Phe
 130 135 140

Tyr Asp Leu Arg Gly Glu Gly Val Lys Leu Gln Val Met Ala Asn Ser
 145 150 155 160

Arg Asn Tyr Lys Ser Glu Glu Glu Phe Ile His Ile Asn Asn Lys Leu
 165 170 175

Arg Arg Gly Asp Ile Ile Gly Val Gln Gly Asn Pro Gly Lys Thr Lys
 180 185 190

Lys Gly Glu Leu Ser Ile Ile Pro Tyr Glu Ile Thr Leu Leu Ser Pro
 195 200 205

Cys Leu His Met Leu Pro His Leu His Phe Gly Leu Lys Asp Lys Glu
 210 215 220

Thr Arg Tyr Arg Gln Arg Tyr Leu Asp Leu Ile Leu Asn Asp Phe Val
 225 230 235 240

Arg Gln Lys Phe Ile Ile Arg Ser Lys Ile Ile Thr Tyr Ile Arg Ser
 245 250 255

Phe Leu Asp Glu Leu Gly Phe Leu Glu Ile Glu Thr Pro Met Met Asn
 260 265 270

Ile Ile Pro Gly Gly Ala Val Ala Lys Pro Phe Ile Thr Tyr His Asn
 275 280 285

Glu Leu Asp Met Asn Leu Tyr Met Arg Ile Ala Pro Glu Leu Tyr His
 290 295 300

Lys Met Leu Val Val Gly Gly Ile Asp Arg Val Tyr Glu Ile Gly Arg
 305 310 315 320

Gln Phe Arg Asn Glu Gly Ile Asp Leu Thr His Asn Pro Glu Phe Thr
325 330 335

Thr Cys Glu Phe Tyr Met Ala Tyr Ala Asp Tyr His Asp Leu Met Glu
340 345 350

Ile Thr Glu Lys Met Val Ser Gly Met Val Lys His Ile Thr Gly Ser
355 360 365

Tyr Lys Val Thr Tyr His Pro Asp Gly Pro Glu Gly Gln Ala Tyr Asp
370 375 380

Val Asp Phe Thr Pro Pro Phe Arg Arg Ile Asn Met Val Glu Glu Leu
385 390 395 400

Glu Lys Ala Leu Gly Met Lys Leu Pro Glu Thr Asn Leu Phe Glu Thr
405 410 415

Glu Glu Thr Arg Lys Ile Leu Asp Asp Ile Cys Val Ala Lys Ala Val
420 425 430

Glu Cys Pro Pro Pro Arg Thr Thr Ala Arg Leu Leu Asp Lys Leu Val
435 440 445

Gly Glu Phe Leu Glu Val Thr Cys Ile Asn Pro Thr Phe Ile Cys Asp
450 455 460

His Pro Gln Ile Met Ser Pro Leu Ala Lys Trp His Arg Ser Lys Glu
465 470 475 480

Gly Leu Thr Glu Arg Phe Glu Leu Phe Val Met Lys Lys Glu Ile Cys
485 490 495

Asn Ala Tyr Thr Glu Leu Asn Asp Pro Met Arg Gln Arg Gln Leu Phe
500 505 510

Glu Glu Gln Ala Lys Ala Lys Ala Ala Gly Asp Asp Glu Ala Met Phe
166/201

515	520	525
Ile Asp Glu Asn Phe Cys Thr Ala Leu Glu Tyr Gly Leu Pro Pro Thr		
530	535	540
Ala Gly Trp Gly Met Gly Ile Asp Arg Val Ala Met Phe Leu Thr Asp		
545	550	555 560
Ser Asn Asn Ile Lys Glu Val Leu Leu Phe Pro Ala Met Lys Pro Glu		
565	570	575
Asp Lys Lys Glu Asn Val Ala Thr Thr Asp Thr Leu Glu Ser Thr Thr		
580	585	590
Val Gly Thr Ser Val		
595		

<210> 57
 <211> 763
 <212> DNA
 <213> Homo sapiens

<400> 57	
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tttacccaaa taaagtatag gcgatagaaa ttgaaacctg gcgcaataga tatagtaccg	120
caagggaag atgaaaaatt ataaccaagc ataatatagc aaggactaac ccctatacct	180
tctgcataat gaattaacta gaaataactt tgcaaggaga gccaaagcta agacccccga	240
aaccagacga gctacctaag aacagctaaa agagcacacc cgtctatgta gcaaaatagt	300
gggaagattt ataggtagag gcgacaaacc taccgagcct ggtgatagct ggttgtccaa	360
gatagaatct tagttcaact ttaaatttgc ccacagaacc ctctaaatcc ccttgtaa	420
ttaactgtta gtccaaagag gaacagctct ttggacacta ggaaaaaacc ttgtagagag	480
agtaaaaaat ttaacaccca tagtaggcct aaaagcagcc accaattaag aaagcgttca	540
agctcaacac ccactaccta aaaaatccca aacatataac tgaactcctc acaccaatt	600
ggaccaatct atcacctat agaagaacta atgttagtat aagtaacatg aaaacattct	660

cctccgcata agcctgcgtc agattaaaac actgaactga caattaacag cccaatatct 720
acaatcaacc cacaagtcac tattaccctc actgtcaacc caa 763

<210> 58
<211> 1575
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (196)..(834)
<223>

<400> 58
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tccccggagc ggagcgcacc tagggtcctt cttccgtccc cccagcccag ctaccggttc 120
agaccagcag cctcgggggg ccccccccg ccagcctgcc tccctcccgc tcagccctgc 180
cagggttccc cagcc atg aat ctc ttc cga ttc ctg gga gac ctc tcc cac 231
Met Asn Leu Phe Arg Phe Leu Gly Asp Leu Ser His
1 5 10
ctc ctc gcc atc atc ttg cta ctg ctc aaa atc tgg aag tcc cgc tcg 279
Leu Leu Ala Ile Ile Leu Leu Leu Leu Lys Ile Trp Lys Ser Arg Ser
15 20 25
tgc gcc gga att tca ggg aag agc cag gtc ctg ttt gct gtg gtg ttc 327
Cys Ala Gly Ile Ser Gly Lys Ser Gln Val Leu Phe Ala Val Val Phe
30 35 40
act gcc cga tat ctg gac ctc ttc acc aac tac atc tca ctc tac aac 375
Thr Ala Arg Tyr Leu Asp Leu Phe Thr Asn Tyr Ile Ser Leu Tyr Asn
45 50 55 60
acg tgt atg aag gtg gtc tac ata gcc tgc tcc ttc acc acg gtc tgg 423
Thr Cys Met Lys Val Val Tyr Ile Ala Cys Ser Phe Thr Thr Val Trp
65 70 75
ttg att tat agc aag ttc aaa gct act tac gat ggg aac cat gac acg 471
Leu Ile Tyr Ser Lys Phe Lys Ala Thr Tyr Asp Gly Asn His Asp Thr
80 85 90
ttc aga gtg gag ttc ctg gtc gtt ccc aca gcc att ctg gcg ttc ctg 519
Phe Arg Val Glu Phe Leu Val Val Pro Thr Ala Ile Leu Ala Phe Leu
95 100 105

gtc aat cat gac ttc acc cct ctg gag atc ctc tgg acc ttc tcc atc	567
Val Asn His Asp Phe Thr Pro Leu Glu Ile Leu Trp Thr Phe Ser Ile	
110 115 120	
tac ctg gag tca gtg gcc atc ttg ccg cag ctg ttc atg gtg agc aag	615
Tyr Leu Glu Ser Val Ala Ile Leu Pro Gln Leu Phe Met Val Ser Lys	
125 130 135 140	
acc ggc gag gcg gag acc atc acc agc cac tac ttg ttt gcg cta ggc	663
Thr Gly Glu Ala Glu Thr Ile Thr Ser His Tyr Leu Phe Ala Leu Gly	
145 150 155	
gtt tac cgc acg ctc tat ctc ttc aac tgg atc tgg cgc tac cat ttc	711
Val Tyr Arg Thr Leu Tyr Leu Phe Asn Trp Ile Trp Arg Tyr His Phe	
160 165 170	
gag ggc ttc ttc gac ctc atc gcc att gtg gca ggc ctg gtc cag aca	759
Glu Gly Phe Phe Asp Leu Ile Ala Ile Val Ala Gly Leu Val Gln Thr	
175 180 185	
gtc ctc tac tgc gat ttc ttc tac ctc tat atc acc aaa gtc cta aag	807
Val Leu Tyr Cys Asp Phe Phe Tyr Leu Tyr Ile Thr Lys Val Leu Lys	
190 195 200	
ggg aag aag ttg agt ttg ccg gca tag ccccggtcct ctccatctct	854
Gly Lys Lys Leu Ser Leu Pro Ala	
205 210	
ctcctcggca gcagcgggag gcagaggaag gcggcagaag atgaagagct ttcccatcca	914
ggggtgactt ttttaagaac ccacctcttg tgctcccat cccgcctcct gccgggtttc	974
agggggacag tggaggatcc aggtcttggg gagctcagga cttgggctgt ttgtagtttt	1034
ttgcctttta gacaagaaaa aaaaatcttt ccactcttta gtttttgatt ctgatgactc	1094
gtttttcttc tactctgttg cccaatttt tataaagtgt ttttgagtgt cctatgggcc	1154
ggggcagggt ccaagatctt ttcccttccc caggcccctc ggctccctcc cagatccac	1214
ccccagcccc actggttgcc aaacactaaa tctgccgaca cccatctgcc ccacctcctg	1274
ccatggccat gaaccgcgac cccactaaa tttctagatt ggggataggg agaaaggag	1334
gcccaggaag gtctcccctg attttttttc atagtaattt ttttcccag agtttgaatt	1394
ttttggtctt ctctgggttt tttggcaaat taggggggcc cggggctcaa gtgcgggaag	1454
ggggctggcc cgaggatccc atggctctca caccatgttt ttgtacagaa ctgatggttg	1514

aatctttgtt ctcttgaaat aaacagaaga aaatgaaacc tttaaaaaaa aaaaaaaaaa 1574

a 1575

<210> 59

<211> 212

<212> PRT

<213> Homo sapiens

<400> 59

Met Asn Leu Phe Arg Phe Leu Gly Asp Leu Ser His Leu Leu Ala Ile
1 5 10 15

Ile Leu Leu Leu Leu Lys Ile Trp Lys Ser Arg Ser Cys Ala Gly Ile
20 25 30

Ser Gly Lys Ser Gln Val Leu Phe Ala Val Val Phe Thr Ala Arg Tyr
35 40 45

Leu Asp Leu Phe Thr Asn Tyr Ile Ser Leu Tyr Asn Thr Cys Met Lys
50 55 60

Val Val Tyr Ile Ala Cys Ser Phe Thr Thr Val Trp Leu Ile Tyr Ser
65 70 75 80

Lys Phe Lys Ala Thr Tyr Asp Gly Asn His Asp Thr Phe Arg Val Glu
85 90 95

Phe Leu Val Val Pro Thr Ala Ile Leu Ala Phe Leu Val Asn His Asp
100 105 110

Phe Thr Pro Leu Glu Ile Leu Trp Thr Phe Ser Ile Tyr Leu Glu Ser
115 120 125

Val Ala Ile Leu Pro Gln Leu Phe Met Val Ser Lys Thr Gly Glu Ala
130 135 140

Glu Thr Ile Thr Ser His Tyr Leu Phe Ala Leu Gly Val Tyr Arg Thr
170/201

145 150 155 160

Leu Tyr Leu Phe Asn Trp Ile Trp Arg Tyr His Phe Glu Gly Phe Phe
165 170 175

Asp Leu Ile Ala Ile Val Ala Gly Leu Val Gln Thr Val Leu Tyr Cys
180 185 190

Asp Phe Phe Tyr Leu Tyr Ile Thr Lys Val Leu Lys Gly Lys Lys Leu
195 200 205

Ser Leu Pro Ala
210

<210> 60
<211> 2245
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (157)..(1110)
<223>

<400> 60
gaatctcgac ccttgaatgg agttacacga acggccagat gaaagaagga aggcccggac 60
ctccactcag ggccgactag gggactggcg gaggggtgcac gctgatggat ttactcaccg 120
ggtgcttggg gctccagcag ctggctggag cccgcg atg acg tca cgg act cgg 174
Met Thr Ser Arg Thr Arg
1 5
gtc aca tgg ccg agt ccg ccc cgc ccc ctc ccc gtc ccc gcc gct gca 222
Val Thr Trp Pro Ser Pro Pro Arg Pro Leu Pro Val Pro Ala Ala Ala
10 15 20
gcc gtc gcc ttc gga gcg aag ggt acc gac ccg gca gaa gct cgg agc 270
Ala Val Ala Phe Gly Ala Lys Gly Thr Asp Pro Ala Glu Ala Arg Ser
25 30 35
tct cgg ggt atc gag gag gca ggc ccg cgg gcg cac ggg cga gcg ggc 318
Ser Arg Gly Ile Glu Glu Ala Gly Pro Arg Ala His Gly Arg Ala Gly
40 45 50

cgg gag ccg gag cgg cgg agg agc cgg cag cag cgg cgc ggc ggg ctc Arg Glu Pro Glu Arg Arg Arg Ser Arg Gln Gln Arg Arg Gly Gly Leu 55 60 65 70	366
cag gcg agg cgg tcg acg ctc ctg aaa act tgc gcg cgc gct cgc gcc Gln Ala Arg Arg Ser Thr Leu Leu Lys Thr Cys Ala Arg Ala Arg Ala 75 80 85	414
act gcg ccc gga gcg atg aag atg gtc gcg ccc tgg acg cgg ttc tac Thr Ala Pro Gly Ala Met Lys Met Val Ala Pro Trp Thr Arg Phe Tyr 90 95 100	462
tcc aac agc tgc tgc ttg tgc tgc cat gtc cgc acc ggc acc atc ctg Ser Asn Ser Cys Cys Leu Cys Cys His Val Arg Thr Gly Thr Ile Leu 105 110 115	510
ctc ggc gtc tgg tat ctg atc atc aat gct gtg gta ctg ttg att tta Leu Gly Val Trp Tyr Leu Ile Ile Asn Ala Val Val Leu Leu Ile Leu 120 125 130	558
ttg agt gcc ctg gct gat ccg gat cag tat aac ttt tca agt tct gaa Leu Ser Ala Leu Ala Asp Pro Asp Gln Tyr Asn Phe Ser Ser Ser Glu 135 140 145 150	606
ctg gga ggt gac ttt gag ttc atg gat gat gcc aac atg tgc att gcc Leu Gly Gly Asp Phe Glu Phe Met Asp Asp Ala Asn Met Cys Ile Ala 155 160 165	654
att gcg att tct ctt ctc atg atc ctg ata tgt gct atg gct act tac Ile Ala Ile Ser Leu Leu Met Ile Leu Ile Cys Ala Met Ala Thr Tyr 170 175 180	702
gga gcg tac aag caa cgc gca gcc tgg atc atc cca ttc ttc tgt tac Gly Ala Tyr Lys Gln Arg Ala Ala Trp Ile Ile Pro Phe Phe Cys Tyr 185 190 195	750
cag atc ttt gac ttt gcc ctg aac atg ttg gtt gca atc act gtg ctt Gln Ile Phe Asp Phe Ala Leu Asn Met Leu Val Ala Ile Thr Val Leu 200 205 210	798
att tat cca aac tcc att cag gaa tac ata cgg caa ctg cct cct aat Ile Tyr Pro Asn Ser Ile Gln Glu Tyr Ile Arg Gln Leu Pro Pro Asn 215 220 225 230	846
ttt ccc tac aga gat gat gtc atg tca gtg aat cct acc tgt ttg gtc Phe Pro Tyr Arg Asp Asp Val Met Ser Val Asn Pro Thr Cys Leu Val 235 240 245	894
ctt att att ctt ctg ttt att agc att atc ttg act ttt aag ggt tac Leu Ile Ile Leu Leu Phe Ile Ser Ile Ile Leu Thr Phe Lys Gly Tyr 172/201	942

250	255	260	
ttg att agc tgt gtt tgg aac tgc tac cga tac atc aat ggt agg aac			990.
Leu Ile Ser Cys Val Trp Asn Cys Tyr Arg Tyr Ile Asn Gly Arg Asn			
265	270	275	
tcc tct gat gtc ctg gtt tat gtt acc agc aat gac act acg gtg ctg			1038
Ser Ser Asp Val Leu Val Tyr Val Thr Ser Asn Asp Thr Thr Val Leu			
280	285	290	
cta ccc ccg tat gat gat gcc act gtg aat ggt gct gcc aag gag cca			1086
Leu Pro Pro Tyr Asp Asp Ala Thr Val Asn Gly Ala Ala Lys Glu Pro			
295	300	305	310
ccg cca cct tac gtg tct gcc taa gccttcaagt gggcggagct gagggcagca			1140
Pro Pro Pro Tyr Val Ser Ala			
315			
gcttgacttt gcagacatct gagcaatagt tctgttatatt cacttttgcc atgagcctct			1200
ctgagcttgt ttgttgctga aatgctactt tttaaaattt agatgtaga ttgaaaactg			1260
tagttttcaa catatgcttt gctggaacac tgtgatagat taactgtaga attcttcctg			1320
tacgattggg gatataatgg gcttcactaa ccttccttag gcattgaaac ttccccaaa			1380
tctgatggac ctagaagtct gcttttgtac ctgctgggcc ccaaagttgg gcatttttct			1440
ctctgttccc tctcttttga aaatgtaaaa taaaaccaa aatagacaac tttttcttca			1500
gccattccag catagagaac aaaaccttat ggaaacagga atgtcaattg tgtaatcatt			1560
gttctaatta ggtaaataga agtccttatg tatgtgttac aagaatttcc cccacaacat			1620
cctttatgac tgaagttcaa tgacagtttg tgtttggtgg taaaggattt tctccatggc			1680
ctgaattaag accattagaa agcaccaggc cgtgggagca gtgaccatct gctgactgtt			1740
cttgtggatc ttgtgtccag ggacatgggg tgacatgcct cgtatgtgtt agagggtgga			1800
atggatgtgt ttggcgctgc atgggatctg gtgccccctt tctcctggat tcacatcccc			1860
accaggggcc cgcttttact aagtgttctg ccctagattg gttcaaggag gtcatccaac			1920
tgactttatc gagtgggaatt gggatatatt tgatatactt ctgcctaaca acatggaaaa			1980
gggttttctt ttccctgcaa gctacatcct actgctttga acttccaagt atgtctagtc			2040
accttttaaa atgtaaacad tttcagaaaa atgaggattg ccttccttgt atgcgctttt			2100

taccttgact acctgaattg caagggattt ttatatattc atatgttaca aagtcagcaa 2160
 ctctcctggtt gggttcattat tgaatgtgct gtaaattaag ttgtttgcaa ttaaaacaag 2220
 gtttgcccac aaaaaaaaaa aaaaa 2245

<210> 61
 <211> 317
 <212> PRT
 <213> Homo sapiens

<400> 61

Met Thr Ser Arg Thr Arg Val Thr Trp Pro Ser Pro Pro Arg Pro Leu
 1 5 10 15

Pro Val Pro Ala Ala Ala Ala Val Ala Phe Gly Ala Lys Gly Thr Asp
 20 25 30

Pro Ala Glu Ala Arg Ser Ser Arg Gly Ile Glu Glu Ala Gly Pro Arg
 35 40 45

Ala His Gly Arg Ala Gly Arg Glu Pro Glu Arg Arg Arg Ser Arg Gln
 50 55 60

Gln Arg Arg Gly Gly Leu Gln Ala Arg Arg Ser Thr Leu Leu Lys Thr
 65 70 75 80

Cys Ala Arg Ala Arg Ala Thr Ala Pro Gly Ala Met Lys Met Val Ala
 85 90 95

Pro Trp Thr Arg Phe Tyr Ser Asn Ser Cys Cys Leu Cys Cys His Val
 100 105 110

Arg Thr Gly Thr Ile Leu Leu Gly Val Trp Tyr Leu Ile Ile Asn Ala
 115 120 125

Val Val Leu Leu Ile Leu Leu Ser Ala Leu Ala Asp Pro Asp Gln Tyr
 130 135 140

Asn Phe Ser Ser Ser Glu Leu Gly Gly Asp Phe Glu Phe Met Asp Asp
145 150 155 160

Ala Asn Met Cys Ile Ala Ile Ala Ile Ser Leu Leu Met Ile Leu Ile
165 170 175

Cys Ala Met Ala Thr Tyr Gly Ala Tyr Lys Gln Arg Ala Ala Trp Ile
180 185 190

Ile Pro Phe Phe Cys Tyr Gln Ile Phe Asp Phe Ala Leu Asn Met Leu
195 200 205

Val Ala Ile Thr Val Leu Ile Tyr Pro Asn Ser Ile Gln Glu Tyr Ile
210 215 220

Arg Gln Leu Pro Pro Asn Phe Pro Tyr Arg Asp Asp Val Met Ser Val
225 230 235 240

Asn Pro Thr Cys Leu Val Leu Ile Ile Leu Leu Phe Ile Ser Ile Ile
245 250 255

Leu Thr Phe Lys Gly Tyr Leu Ile Ser Cys Val Trp Asn Cys Tyr Arg
260 265 270

Tyr Ile Asn Gly Arg Asn Ser Ser Asp Val Leu Val Tyr Val Thr Ser
275 280 285

Asn Asp Thr Thr Val Leu Leu Pro Pro Tyr Asp Asp Ala Thr Val Asn
290 295 300

Gly Ala Ala Lys Glu Pro Pro Pro Pro Tyr Val Ser Ala
305 310 315

<210> 62
<211> 1453
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
 <222> (65).. (1057)
 <223>

<400> 62
 ggctgccgga gggcgggagg caggagcggg ccaggagctg ctgggctgga gcggcggcgc 60
 cgcc atg tcc gac agc gag aag ctc aac ctg gac tcg atc atc ggg cgc 109
 Met Ser Asp Ser Glu Lys Leu Asn Leu Asp Ser Ile Ile Gly Arg
 1 5 10 15
 ctg ctg gaa gtg cag ggc tcg cgg cct ggc aag aat gta cag ctg aca 157
 Leu Leu Glu Val Gln Gly Ser Arg Pro Gly Lys Asn Val Gln Leu Thr
 20 25 30
 gag aac gag atc cgc ggt ctg tgc ctg aaa tcc cgg gag att ttt ctg 205
 Glu Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile Phe Leu
 35 40 45
 agc cag ccc att ctt ctg gag ctg gag gca ccc ctc aag atc tgc ggt 253
 Ser Gln Pro Ile Leu Leu Glu Leu Glu Ala Pro Leu Lys Ile Cys Gly
 50 55 60
 gac ata cac ggc cag tac tac gac ctt ctg cga cta ttt gag tat ggc 301
 Asp Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly
 65 70 75
 ggt ttc cct ccc gag agc aac tac ctc ttt ctg ggg gac tat gtg gac 349
 Gly Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp
 80 85 90 95
 agg ggc aag cag tcc ttg gag acc atc tgc ctg ctg ctg gcc tat aag 397
 Arg Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Leu Ala Tyr Lys
 100 105 110
 atc aag tac ccc gag aac ttc ttc ctg ctc cgt ggg aac cac gag tgt 445
 Ile Lys Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys
 115 120 125
 gcc agc atc aac cgc atc tat ggt ttc tac gat gag tgc aag aga cgc 493
 Ala Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg
 130 135 140
 tac aac atc aaa ctg tgg aaa acc ttc act gac tgc ttc aac tgc ctg 541
 Tyr Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu
 145 150 155
 ccc atc gcg gcc ata gtg gac gaa aag atc ttc tgc tgc cac gga ggc 589
 Pro Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly
 160 165 170 175

ctg tcc ccg gac ctg cag tct atg gag cag att cgg cgg atc atg cgg	637
Leu Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg	
180 185 190	
ccc aca gat gtg cct gac cag ggc ctg ctg tgt gac ctg ctg tgg tct	685
Pro Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser	
195 200 205	
gac cct gac aag gac gtg cag ggc tgg ggc gag aac gac cgt ggc gtc	733
Asp Pro Asp Lys Asp Val Gln Gly Trp Gly Glu Asn Asp Arg Gly Val	
210 215 220	
tct ttt acc ttt gga gcc gag gtg gtg gcc aag ttc ctc cac aag cac	781
Ser Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His	
225 230 235	
gac ttg gac ctc atc tgc cga gca cac cag gtg gta gaa gac ggc tac	829
Asp Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr	
240 245 250 255	
gag ttc ttt gcc aag cgg cag ctg gtg aca ctt ttc tca gct ccc aac	877
Glu Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn	
260 265 270	
tac tgt ggc gag ttt gac aat gct ggc gcc atg atg agt gtg gac gag	925
Tyr Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu	
275 280 285	
acc ctc atg tgc tct ttc cag atc ctc aag ccc gcc gac aag aac aag	973
Thr Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Asp Lys Asn Lys	
290 295 300	
ggg aag tac ggg cag ttc agt ggc ctg aac cct gga ggc cga ccc atc	1021
Gly Lys Tyr Gly Gln Phe Ser Gly Leu Asn Pro Gly Gly Arg Pro Ile	
305 310 315	
acc cca ccc cgc aat tcc gcc aaa gcc aag aaa tag cccccgcaca	1067
Thr Pro Pro Arg Asn Ser Ala Lys Ala Lys Lys	
320 325 330	
ccaccctgtg cccagatga tggattgatt gtacagaaat catgctgcca tgctgggggg	1127
gggtcacccc gaccctcag gccacctgt cacggggaac atggagcctt ggtgtatttt	1187
tcttttcttt ttttaatgaa tcaatagcag cgtccagtcc cccagggctg cttcctgcct	1247
gcacctgcgg tgactgtgag caggatcctg gggccgaggc tgcagctcag ggcaacggca	1307
ggccaggctcg tgggtctcca gccgtgcttg gcctcagggc tggcagccgg atcctggggc	1367

aacccatctg gtctcttgaa taaaggtcaa agctggattc tcaaaaaaaaaa aaaaaaaaaa 1427
 aaaaaaaaaa aaaaaaaaaa aaaaaa 1453

<210> 63
 <211> 330
 <212> PRT
 <213> Homo sapiens

<400> 63

Met Ser Asp Ser Glu Lys Leu Asn Leu Asp Ser Ile Ile Gly Arg Leu
 1 5 10 15

Leu Glu Val Gln Gly Ser Arg Pro Gly Lys Asn Val Gln Leu Thr Glu
 20 25 30

Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile Phe Leu Ser
 35 40 45

Gln Pro Ile Leu Leu Glu Leu Glu Ala Pro Leu Lys Ile Cys Gly Asp
 50 55 60

Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly
 65 70 75 80

Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg
 85 90 95

Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Leu Ala Tyr Lys Ile
 100 105 110

Lys Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala
 115 120 125

Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr
 130 135 140

Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro
 178/201

145	150	155	160
Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu	165	170	175
Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro	180	185	190
Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp	195	200	205
Pro Asp Lys Asp Val Gln Gly Trp Gly Glu Asn Asp Arg Gly Val Ser	210	215	220
Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp	225	230	235
Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu	245	250	255
Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr	260	265	270
Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr	275	280	285
Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Asp Lys Asn Lys Gly	290	295	300
Lys Tyr Gly Gln Phe Ser Gly Leu Asn Pro Gly Gly Arg Pro Ile Thr	305	310	315
Pro Pro Arg Asn Ser Ala Lys Ala Lys Lys	325	330	

<210> 64
 <211> 1591
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (44)..(814)

<223>

<400> 64

ccctgcgtct ctgcccgcgc cgtggcgcgc gagtgcactg aag atg gcg gct gct	55
Met Ala Ala Ala	
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gta gga cgg ttg ctc cga gcg tcg gtt gcc cga cat gtg agt gcc att	103
Val Gly Arg Leu Leu Arg Ala Ser Val Ala Arg His Val Ser Ala Ile	
5 10 15 20	
cct tgg ggc att tct gcc act gca gcc ctc agg cct gct gca tgt gga	151
Pro Trp Gly Ile Ser Ala Thr Ala Ala Leu Arg Pro Ala Ala Cys Gly	
25 30 35	
aga acg agc ttg aca aat tta ttg tgt tct ggt tcc agt caa gca aaa	199
Arg Thr Ser Leu Thr Asn Leu Leu Cys Ser Gly Ser Ser Gln Ala Lys	
40 45 50	
tta ttc agc acc agt tcc tca tgc cat gca cct gct gtc acc cag cat	247
Leu Phe Ser Thr Ser Ser Ser Cys His Ala Pro Ala Val Thr Gln His	
55 60 65	
gca ccc tat ttt aag ggt aca gcc gtt gtc aat gga gag ttc aaa gac	295
Ala Pro Tyr Phe Lys Gly Thr Ala Val Val Asn Gly Glu Phe Lys Asp	
70 75 80	
cta agc ctt gat gac ttt aag ggg aaa tat ttg gtg ctt ttc ttc tat	343
Leu Ser Leu Asp Asp Phe Lys Gly Lys Tyr Leu Val Leu Phe Phe Tyr	
85 90 95 100	
cct ttg gat ttc acc ttt gtg tgt cct aca gaa att gtt gct ttt agt	391
Pro Leu Asp Phe Thr Phe Val Cys Pro Thr Glu Ile Val Ala Phe Ser	
105 110 115	
gac aaa gct aac gaa ttt cac gac gtg aac tgt gaa gtt gtc gca gtc	439
Asp Lys Ala Asn Glu Phe His Asp Val Asn Cys Glu Val Val Ala Val	
120 125 130	
tca gtg gat tcc cac ttt agc cat ctt gcc tgg ata aat aca cca agg	487
Ser Val Asp Ser His Phe Ser His Leu Ala Trp Ile Asn Thr Pro Arg	
135 140 145	
aag aat ggt ggt ttg ggc cac atg aac atc gca ctc ttg tca gac tta	535
Lys Asn Gly Gly Leu Gly His Met Asn Ile Ala Leu Leu Ser Asp Leu	

150	155	160	
act aag cag att tcc cga gac tac ggt gtg ctg tta gaa ggt tct ggt			583
Thr Lys Gln Ile Ser Arg Asp Tyr Gly Val Leu Leu Glu Gly Ser Gly			
165	170	175	180
ctt gca cta aga ggt ctc ttc ata att gac ccc aat gga gtc atc aag			631
Leu Ala Leu Arg Gly Leu Phe Ile Ile Asp Pro Asn Gly Val Ile Lys			
	185	190	195
cat ttg agc gtc aac gat ctc cca gtg ggc cga agc gtg gaa gaa acc			679
His Leu Ser Val Asn Asp Leu Pro Val Gly Arg Ser Val Glu Glu Thr			
	200	205	210
ctc cgc ttg gtg aag gcg ttc cag tat gta gaa aca cat gga gaa gtc			727
Leu Arg Leu Val Lys Ala Phe Gln Tyr Val Glu Thr His Gly Glu Val			
	215	220	225
tgc cca gcg aac tgg aca ccg gat tct cct acg atc aag cca agt cca			775
Cys Pro Ala Asn Trp Thr Pro Asp Ser Pro Thr Ile Lys Pro Ser Pro			
	230	235	240
gct gct tcc aaa gag tac ttt cag aag gta aat cag tag atcacccatg			824
Ala Ala Ser Lys Glu Tyr Phe Gln Lys Val Asn Gln			
245	250	255	
tgtatctgca ccttctcaac tgagagaaga accacagttg aaacctgctt ttatcatttt			884
caagatgggtt atttgtagaa ggcaaggaac caattatgct tgtattcata agtattactc			944
taaatgtttt gtttttgtaa ttctggctaa gaccttttaa acatgggttag ttgctagtag			1004
aaggaatcct ttattggtaa catcttggtg gctggctagc tagtttctac agaacataat			1064
ttgcctctat agaaggctat tcttagatca tgtctcaatg gaaacactct tctttcttag			1124
ccttacttga atcttgcccta taataaagta gagcaacaca cattgaaagc ttctgatcaa			1184
cggtcctgaa attttcatct tgaatgtctt tgtattaaac tgaattttct ttttaagctaa			1244
caaagatcat aattttcaat gattagccgt gtaactcctg caatgaatgt ttatgtgatt			1304
gaagcaaagtg tgaatcgtat tatttttaaaa agtggcagag tgacttaact gatcatgcat			1364
gatecctcat ccctgaaatt gagtttatgt agtcatttta cttattttat tcattagcta			1424
actttgtcta tgtatatattc tagatatatga ttagtgtaat cgattataaa ggatatttat			1484
caaatccagg gattgcattt tgaaattata attattttct ttgctgaagt attcattgta			1544

aaacatacaa aataaacata ttttaaaaca ttgtcatttt accacca

1591

<210> 65
<211> 256
<212> PRT
<213> Homo sapiens

<400> 65

Met Ala Ala Ala Val Gly Arg Leu Leu Arg Ala Ser Val Ala Arg His
1 5 10 15

Val Ser Ala Ile Pro Trp Gly Ile Ser Ala Thr Ala Ala Leu Arg Pro
20 25 30

Ala Ala Cys Gly Arg Thr Ser Leu Thr Asn Leu Leu Cys Ser Gly Ser
35 40 45

Ser Gln Ala Lys Leu Phe Ser Thr Ser Ser Ser Cys His Ala Pro Ala
50 55 60

Val Thr Gln His Ala Pro Tyr Phe Lys Gly Thr Ala Val Val Asn Gly
65 70 75 80

Glu Phe Lys Asp Leu Ser Leu Asp Asp Phe Lys Gly Lys Tyr Leu Val
85 90 95

Leu Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys Pro Thr Glu Ile
100 105 110

Val Ala Phe Ser Asp Lys Ala Asn Glu Phe His Asp Val Asn Cys Glu
115 120 125

Val Val Ala Val Ser Val Asp Ser His Phe Ser His Leu Ala Trp Ile
130 135 140

Asn Thr Pro Arg Lys Asn Gly Gly Leu Gly His Met Asn Ile Ala Leu
145 150 155 160

Leu Ser Asp Leu Thr Lys Gln Ile Ser Arg Asp Tyr Gly Val Leu Leu
165 170 175

Glu Gly Ser Gly Leu Ala Leu Arg Gly Leu Phe Ile Ile Asp Pro Asn
180 185 190

Gly Val Ile Lys His Leu Ser Val Asn Asp Leu Pro Val Gly Arg Ser
195 200 205

Val Glu Glu Thr Leu Arg Leu Val Lys Ala Phe Gln Tyr Val Glu Thr
210 215 220

His Gly Glu Val Cys Pro Ala Asn Trp Thr Pro Asp Ser Pro Thr Ile
225 230 235 240

Lys Pro Ser Pro Ala Ala Ser Lys Glu Tyr Phe Gln Lys Val Asn Gln
245 250 255

<210> 66
<211> 1224
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (70)..(1041)
<223>

<400> 66
gccattgtt tttgtaatct ctgaggagaa gcagcagcaa acatttgcta gtcagacaag 60
tgacaggga atg gat tcc aaa cac cag tgt gta aag cta aat gat ggc cac 111
Met Asp Ser Lys His Gln Cys Val Lys Leu Asn Asp Gly His
1 5 10
ttc atg cct gta ttg gga ttt ggc acc tat gca cct cca gag gtt ccg 159
Phe Met Pro Val Leu Gly Phe Gly Thr Tyr Ala Pro Pro Glu Val Pro
15 20 25 30
aga agt aaa gct ttg gag gtc aca aaa tta gca ata gaa gct ggg ttc 207
Arg Ser Lys Ala Leu Glu Val Thr Lys Leu Ala Ile Glu Ala Gly Phe
35 40 45
cgc cat ata gat tct gct cat tta tac aat aat gag gag cag gtt gga 255
183/201

Arg	His	Ile	Asp	Ser	Ala	His	Leu	Tyr	Asn	Asn	Glu	Glu	Gln	Val	Gly		
			50					55					60				
ctg	gcc	atc	cga	agc	aag	att	gca	gat	ggc	agt	gtg	aag	aga	gaa	gac	303	
Leu	Ala	Ile	Arg	Ser	Lys	Ile	Ala	Asp	Gly	Ser	Val	Lys	Arg	Glu	Asp		
		65					70					75					
ata	ttc	tac	act	tca	aag	ctt	tgg	tcc	act	ttt	cat	cga	cca	gag	ttg	351	
Ile	Phe	Tyr	Thr	Ser	Lys	Leu	Trp	Ser	Thr	Phe	His	Arg	Pro	Glu	Leu		
	80					85					90						
gtc	cga	cca	gcc	ttg	gaa	aac	tca	ctg	aag	aaa	gct	caa	ttg	gac	tat	399	
Val	Arg	Pro	Ala	Leu	Glu	Asn	Ser	Leu	Lys	Lys	Ala	Gln	Leu	Asp	Tyr		
95					100				105						110		
gtt	gac	ctc	tat	ctt	att	cat	tct	cca	atg	tct	cta	aag	cca	ggt	gag	447	
Val	Asp	Leu	Tyr	Leu	Ile	His	Ser	Pro	Met	Ser	Leu	Lys	Pro	Gly	Glu		
				115				120						125			
gaa	ctt	tca	cca	aca	gat	gaa	aat	gga	aaa	gta	ata	ttt	gac	ata	gtg	495	
Glu	Leu	Ser	Pro	Thr	Asp	Glu	Asn	Gly	Lys	Val	Ile	Phe	Asp	Ile	Val		
			130					135					140				
gat	ctc	tgt	acc	acc	tgg	gag	gcc	atg	gag	aag	tgt	aag	gat	gca	gga	543	
Asp	Leu	Cys	Thr	Thr	Trp	Glu	Ala	Met	Glu	Lys	Cys	Lys	Asp	Ala	Gly		
		145				150						155					
ttg	gcc	aag	tcc	att	ggg	gtg	tca	aac	ttc	aac	cgc	agg	cag	ctg	gag	591	
Leu	Ala	Lys	Ser	Ile	Gly	Val	Ser	Asn	Phe	Asn	Arg	Arg	Gln	Leu	Glu		
	160					165					170						
atg	atc	ctc	aac	aag	cca	gga	ctc	aag	tac	aag	cct	gtc	tgc	aac	cag	639	
Met	Ile	Leu	Asn	Lys	Pro	Gly	Leu	Lys	Tyr	Lys	Pro	Val	Cys	Asn	Gln		
175					180					185					190		
gta	gaa	tgt	cat	ccg	tat	ttc	aac	cgg	agt	aaa	ttg	cta	gat	ttc	tgc	687	
Val	Glu	Cys	His	Pro	Tyr	Phe	Asn	Arg	Ser	Lys	Leu	Leu	Asp	Phe	Cys		
				195				200						205			
aag	tcg	aaa	gat	att	gtt	ctg	gtt	gcc	tat	agt	gct	ctg	gga	tct	caa	735	
Lys	Ser	Lys	Asp	Ile	Val	Leu	Val	Ala	Tyr	Ser	Ala	Leu	Gly	Ser	Gln		
			210					215					220				
cga	gac	aaa	cga	tgg	gtg	gac	ccg	aac	tcc	ccg	gtg	ctc	ttg	gag	gac	783	
Arg	Asp	Lys	Arg	Trp	Val	Asp	Pro	Asn	Ser	Pro	Val	Leu	Leu	Glu	Asp		
		225					230					235					
cca	gtc	ctt	tgt	gcc	ttg	gca	aaa	aag	cac	aag	cga	acc	cca	gcc	ctg	831	
Pro	Val	Leu	Cys	Ala	Leu	Ala	Lys	Lys	His	Lys	Arg	Thr	Pro	Ala	Leu		
	240					245					250						

att gcc ctg cgc tac cag ctg cag cgt ggg gtt gtg gtc ctg gcc aag 879
 Ile Ala Leu Arg Tyr Gln Leu Gln Arg Gly Val Val Val Leu Ala Lys
 255 260 265 270

agc tac aat gag cag cgc atc aga cag aac gtg cag gtt ttt gag ttc 927
 Ser Tyr Asn Glu Gln Arg Ile Arg Gln Asn Val Gln Val Phe Glu Phe
 275 280 285

cag ttg act gca gag gac atg aaa gcc ata gat ggc cta gac aga aat 975
 Gln Leu Thr Ala Glu Asp Met Lys Ala Ile Asp Gly Leu Asp Arg Asn
 290 295 300

ctc cac tat ttt aac agt gat agt ttt gct agc cac cct aat tat cca 1023
 Leu His Tyr Phe Asn Ser Asp Ser Phe Ala Ser His Pro Asn Tyr Pro
 305 310 315

tat tca gat gaa tat taa catggagggc tttgcctgat gtctaccaga 1071
 Tyr Ser Asp Glu Tyr
 320

agccctgtgt gtggatgggtg acgcagagga cgtctctatg ccggtgactg gacatatcac 1131

ctctacttaa atccgtcctg tttagecgact tcagtcaact acagctgagt ccataggcca 1191

gaaagacaat aaatttttat cattttgaaa taa 1224

<210> 67
 <211> 323
 <212> PRT
 <213> Homo sapiens

<400> 67

Met Asp Ser Lys His Gln Cys Val Lys Leu Asn Asp Gly His Phe Met
 1 5 10 15

Pro Val Leu Gly Phe Gly Thr Tyr Ala Pro Pro Glu Val Pro Arg Ser
 20 25 30

Lys Ala Leu Glu Val Thr Lys Leu Ala Ile Glu Ala Gly Phe Arg His
 35 40 45

Ile Asp Ser Ala His Leu Tyr Asn Asn Glu Glu Gln Val Gly Leu Ala
 50 55 60

Ile Arg Ser Lys Ile Ala Asp Gly Ser Val Lys Arg Glu Asp Ile Phe
65 70 75 80

Tyr Thr Ser Lys Leu Trp Ser Thr Phe His Arg Pro Glu Leu Val Arg
85 90 95

Pro Ala Leu Glu Asn Ser Leu Lys Lys Ala Gln Leu Asp Tyr Val Asp
100 105 110

Leu Tyr Leu Ile His Ser Pro Met Ser Leu Lys Pro Gly Glu Glu Leu
115 120 125

Ser Pro Thr Asp Glu Asn Gly Lys Val Ile Phe Asp Ile Val Asp Leu
130 135 140

Cys Thr Thr Trp Glu Ala Met Glu Lys Cys Lys Asp Ala Gly Leu Ala
145 150 155 160

Lys Ser Ile Gly Val Ser Asn Phe Asn Arg Arg Gln Leu Glu Met Ile
165 170 175

Leu Asn Lys Pro Gly Leu Lys Tyr Lys Pro Val Cys Asn Gln Val Glu
180 185 190

Cys His Pro Tyr Phe Asn Arg Ser Lys Leu Leu Asp Phe Cys Lys Ser
195 200 205

Lys Asp Ile Val Leu Val Ala Tyr Ser Ala Leu Gly Ser Gln Arg Asp
210 215 220

Lys Arg Trp Val Asp Pro Asn Ser Pro Val Leu Leu Glu Asp Pro Val
225 230 235 240

Leu Cys Ala Leu Ala Lys Lys His Lys Arg Thr Pro Ala Leu Ile Ala
245 250 255

Leu Arg Tyr Gln Leu Gln Arg Gly Val Val Val Leu Ala Lys Ser Tyr
186/201

260

265

270

Asn Glu Gln Arg Ile Arg Gln Asn Val Gln Val Phe Glu Phe Gln Leu
 275 280 285

Thr Ala Glu Asp Met Lys Ala Ile Asp Gly Leu Asp Arg Asn Leu His
 290 295 300

Tyr Phe Asn Ser Asp Ser Phe Ala Ser His Pro Asn Tyr Pro Tyr Ser
 305 310 315 320

Asp Glu Tyr

<210> 68
 <211> 1715
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (37)..(591)
 <223>

<400> 68
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 Met Ser Gly Ile Ala Leu
 1 5

agc aga ctc gcc cag gag agg aaa gca tgg agg aaa gac cac cca ttt 102
 Ser Arg Leu Ala Gln Glu Arg Lys Ala Trp Arg Lys Asp His Pro Phe
 10 15 20

ggt ttc gtg gct gtc cca aca aaa aat ccc gat ggc acg atg aac ctc 150
 Gly Phe Val Ala Val Pro Thr Lys Asn Pro Asp Gly Thr Met Asn Leu
 25 30 35

atg aac tgg gag tgc gcc att cca gga aag aaa ggg act ccg tgg gaa 198
 Met Asn Trp Glu Cys Ala Ile Pro Gly Lys Lys Gly Thr Pro Trp Glu
 40 45 50

gga ggc ttg ttt aaa cta cgg atg ctt ttc aaa gat gat tat cca tct 246
 Gly Gly Leu Phe Lys Leu Arg Met Leu Phe Lys Asp Asp Tyr Pro Ser
 55 60 65 70

tcg cca cca aaa tgt aaa ttc gaa cca cca tta ttt cac ccg aat gtg	294
Ser Pro Pro Lys Cys Lys Phe Glu Pro Pro Leu Phe His Pro Asn Val	
75 80 85	
tac cct tcg ggg aca gtg tgc ctg tcc atc tta gag gag gac aag gac	342
Tyr Pro Ser Gly Thr Val Cys Leu Ser Ile Leu Glu Glu Asp Lys Asp	
90 95 100	
tgg agg cca gcc atc aca atc aaa cag atc cta tta gga ata cag gaa	390
Trp Arg Pro Ala Ile Thr Ile Lys Gln Ile Leu Leu Gly Ile Gln Glu	
105 110 115	
ctt cta aat gaa cca aat atc caa gac cca gct caa gca gag gcc tac	438
Leu Leu Asn Glu Pro Asn Ile Gln Asp Pro Ala Gln Ala Glu Ala Tyr	
120 125 130	
acg att tac tgg tta gta gca gcc ctg gcc ccg ctg gtg gca gct cct	486
Thr Ile Tyr Trp Leu Val Ala Ala Leu Ala Pro Leu Val Ala Ala Pro	
135 140 145 150	
ccc cgt ccc agc caa ggc cgc ctg gca gga cgg gag tgg agc aca cag	534
Pro Arg Pro Ser Gln Gly Arg Leu Ala Gly Arg Glu Trp Ser Thr Gln	
155 160 165	
gct cac cct agg gac agc cag ggt ccg cgc ctc tgt ggg gaa ggt cgg	582
Ala His Pro Arg Asp Ser Gln Gly Pro Arg Leu Cys Gly Glu Gly Arg	
170 175 180	
ggg gca taa accctgtggg cagcaggcac cggtgcacac cgctctgcggt	631
Gly Ala	
gggcatggat ggcgccggag ccgtgtccag gggagggagc aggccagggtg acaggggctg	691
tcttgggcca ctgccccagt gagttgtggc cagctaggag gggaaggacc ctgggcgtgg	751
gtgccagagg aggccatgct gagaggcctc tccaccggct cagcctcccg tggaccccag	811
cctcccgcgc cgcccttgct gcttgctccc atcccctcta caacttggtt ccttctgtgg	871
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ccctgtccct gtgaggtgct gctgtggcta gaagggtccc cgtgggcctg gggtcctgtc	991
tgcaccgagg agggcctggt gtgagttagg atgcagacga cagccaaaca gtgctgggga	1051
aagcagggag gaccctgccc tgagcagagg ccatgcgccc gcctgtcctg ttcctctgc	1111
agctgttctg ggcagggtcca taagaagggtg gggtggggcc tccgaccccc actgctccgc	1171

ctgcagggtt gagaaacca gcccacatct accacgggtc cccacacctc tgaggaggtc 1231
tcagggtccc caatggccag ggaccacaga ggctcacctg cagccacccc acacatccct 1291
gccactgtgg gcatcagagg ccctctccct ccagggtgca tctcctggtc aggagggggg 1351
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aaaa 1715

<210> 69
<211> 184
<212> PRT
<213> Homo sapiens

<400> 69

Met Ser Gly Ile Ala Leu Ser Arg Leu Ala Gln Glu Arg Lys Ala Trp
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Arg Lys Asp His Pro Phe Gly Phe Val Ala Val Pro Thr Lys Asn Pro
20 25 30

Asp Gly Thr Met Asn Leu Met Asn Trp Glu Cys Ala Ile Pro Gly Lys
35 40 45

Lys Gly Thr Pro Trp Glu Gly Gly Leu Phe Lys Leu Arg Met Leu Phe
50 55 60

Lys Asp Asp Tyr Pro Ser Ser Pro Pro Lys Cys Lys Phe Glu Pro Pro
65 70 75 80

Leu Phe His Pro Asn Val Tyr Pro Ser Gly Thr Val Cys Leu Ser Ile
85 90 95

Leu Glu Glu Asp Lys Asp Trp Arg Pro Ala Ile Thr Ile Lys Gln Ile
100 105 110

Leu Leu Gly Ile Gln Glu Leu Leu Asn Glu Pro Asn Ile Gln Asp Pro
115 120 125

Ala Gln Ala Glu Ala Tyr Thr Ile Tyr Trp Leu Val Ala Ala Leu Ala
130 135 140

Pro Leu Val Ala Ala Pro Pro Arg Pro Ser Gln Gly Arg Leu Ala Gly
145 150 155 160

Arg Glu Trp Ser Thr Gln Ala His Pro Arg Asp Ser Gln Gly Pro Arg
165 170 175

Leu Cys Gly Glu Gly Arg Gly Ala
180

<210> 70
<211> 1327
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (100).. (966)
<223>

<400> 70
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cgggacgcgc tgggaccggc gtcgggggtc gcggggacc atg cag cgg agg tgg 114
Met Gln Arg Arg Trp
1 5

gtc ttc gtg ctg ctc gac gtg ctg tgc tta ctg gtc gcc tcc ctg ccc 162
Val Phe Val Leu Leu Asp Val Leu Cys Leu Leu Val Ala Ser Leu Pro
10 15 20

ttc gct atc ctg acg ctg gtg aac gcc ccg tac aag cga gga ttt tac 210
Phe Ala Ile Leu Thr Leu Val Asn Ala Pro Tyr Lys Arg Gly Phe Tyr
25 30 35

tgc ggg gat gac tcc atc cgg tac ccc tac cgt cca gat acc atc acc Cys Gly Asp Asp Ser Ile Arg Tyr Pro Tyr Arg Pro Asp Thr Ile Thr 40 45 50	258
cac ggg ctc atg gct ggg gtc acc atc acg gcc acc gtc atc ctt gtc His Gly Leu Met Ala Gly Val Thr Ile Thr Ala Thr Val Ile Leu Val 55 60 65	306
tgc gcc ggg gaa gcc tac ctg gtg tac aca gac cgg ctc tat tct cgc Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr Asp Arg Leu Tyr Ser Arg 70 75 80 85	354
tgc gac ttc aac aac tac gtg gct gct gta tac aag gtg ctg ggg acc Ser Asp Phe Asn Asn Tyr Val Ala Ala Val Tyr Lys Val Leu Gly Thr 90 95 100	402
ttc ctg ttt ggg gct gcc gtg agc cag tct ctg aca gac ctg gcc aag Phe Leu Phe Gly Ala Ala Val Ser Gln Ser Leu Thr Asp Leu Ala Lys 105 110 115	450
tac atg att ggg cgt ctg agg ccc aac ttc cta gcc gtc tgc gac ccc Tyr Met Ile Gly Arg Leu Arg Pro Asn Phe Leu Ala Val Cys Asp Pro 120 125 130	498
gac tgg agc cgg gtc aac tgc tgc gtc tat gtg cag ctg gag aag gtg Asp Trp Ser Arg Val Asn Cys Ser Val Tyr Val Gln Leu Glu Lys Val 135 140 145	546
tgc agg gga aac cct gct gat gtc acc gag gcc agg ttg tct ttc tac Cys Arg Gly Asn Pro Ala Asp Val Thr Glu Ala Arg Leu Ser Phe Tyr 150 155 160 165	594
tgc gga cac tct tcc ttt ggg atg tac tgc atg gtg ttc ttg gcg ctg Ser Gly His Ser Ser Phe Gly Met Tyr Cys Met Val Phe Leu Ala Leu 170 175 180	642
tat gtg cag gca cga ctc tgt tgg aag tgg gca cgg ctg ctg cga ccc Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp Ala Arg Leu Leu Arg Pro 185 190 195	690
aca gtc cag ttc ttc ctg gtg gcc ttt gcc ctc tac gtg ggc tac acc Thr Val Gln Phe Phe Leu Val Ala Phe Ala Leu Tyr Val Gly Tyr Thr 200 205 210	738
cgc gtg tct gat tac aaa cac cac tgg agc gat gtc ctt gtt ggc ctc Arg Val Ser Asp Tyr Lys His His Trp Ser Asp Val Leu Val Gly Leu 215 220 225	786
ctg cag ggg gca ctg gtg gct gcc ctc act gtc tgc tac atc tca gac 191/201	834

Leu	Gln	Gly	Ala	Leu	Val	Ala	Ala	Leu	Thr	Val	Cys	Tyr	Ile	Ser	Asp	
230					235					240					245	
ttc	ttc	aaa	gcc	cga	ccc	cca	cag	cac	tgt	ctg	aag	gag	gag	gag	ctg	882
Phe	Phe	Lys	Ala	Arg	Pro	Pro	Gln	His	Cys	Leu	Lys	Glu	Glu	Glu	Leu	
			250					255						260		
gaa	cgg	aag	ccc	agc	ctg	tca	ctg	acg	ttg	acc	ctg	ggc	gag	gct	gac	930
Glu	Arg	Lys	Pro	Ser	Leu	Ser	Leu	Thr	Leu	Thr	Leu	Gly	Glu	Ala	Asp	
			265					270					275			
cac	aac	cac	tat	gga	tac	ccg	cac	tcc	tcc	tcc	tga	ggccggaccc				976
His	Asn	His	Tyr	Gly	Tyr	Pro	His	Ser	Ser	Ser						
	280						285									
cgcccaggca	gggagctgct	gtgagtcacag	ctgaggccca	cccagggtggt	ccctccagcc											1036
ctggtttaggc	actgagggct	ctggacgggc	tccaggaacc	ctgggctgat	gggagcagtg											1096
agcgggctcc	gctgccccct	gccctgcact	ggaccaggag	tctggagatg	cctgggtagc											1156
cctcagcatt	tggaggggaa	cctgttcccg	tcggtcacca	aatatcccct	tctttttatg											1216
gggttaagga	agggaccgag	agatcagata	gttgctgttt	tgtaaaatgt	aatgtatatg											1276
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<210> 71
 <211> 288
 <212> PRT
 <213> Homo sapiens

<400> 71

Met	Gln	Arg	Arg	Trp	Val	Phe	Val	Leu	Leu	Asp	Val	Leu	Cys	Leu	Leu
1				5				10					15		

Val	Ala	Ser	Leu	Pro	Phe	Ala	Ile	Leu	Thr	Leu	Val	Asn	Ala	Pro	Tyr
			20					25					30		

Lys	Arg	Gly	Phe	Tyr	Cys	Gly	Asp	Asp	Ser	Ile	Arg	Tyr	Pro	Tyr	Arg
		35					40					45			

Pro	Asp	Thr	Ile	Thr	His	Gly	Leu	Met	Ala	Gly	Val	Thr	Ile	Thr	Ala
	50					55					60				

Thr Val Ile Leu Val Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr Asp
65 70 75 80

Arg Leu Tyr Ser Arg Ser Asp Phe Asn Asn Tyr Val Ala Ala Val Tyr
85 90 95

Lys Val Leu Gly Thr Phe Leu Phe Gly Ala Ala Val Ser Gln Ser Leu
100 105 110

Thr Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Arg Pro Asn Phe Leu
115 120 125

Ala Val Cys Asp Pro Asp Trp Ser Arg Val Asn Cys Ser Val Tyr Val
130 135 140

Gln Leu Glu Lys Val Cys Arg Gly Asn Pro Ala Asp Val Thr Glu Ala
145 150 155 160

Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys Met
165 170 175

Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp Ala
180 185 190

Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala Leu
195 200 205

Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser Asp
210 215 220

Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr Val
225 230 235 240

Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys Leu
245 250 255

Lys Glu Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu Thr
193/201

260

265

270

Leu Gly Glu Ala Asp His Asn His Tyr Gly Tyr Pro His Ser Ser Ser
 275 280 285

<210> 72
 <211> 2980
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (274).. (519)
 <223>

<220>
 <221> misc_feature
 <222> (2974).. (2974)
 <223> n = a, t, g or c

<400> 72
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 ggaacaggcc gccgcgcgct gcgcgccgga cccgctgccc ctgccggccc ggccgggtcg 120
 ggccggcccag ggaccgacag acttgacaac ggtgacagca ctggggcggc accttcctac 180
 ttctgcccag ccacagccct cccctcacag ttgagcacct gtttgccctga agttaatttc 240
 cagaagcagg agtccccaga gccaggcagg ggg atg aac cgc gag gga gct ccc 294
 Met Asn Arg Glu Gly Ala Pro
 1 5
 ggg aag agt ccg gag gag atg tac att cag cag aag gtc cga gtg ctg 342
 Gly Lys Ser Pro Glu Glu Met Tyr Ile Gln Gln Lys Val Arg Val Leu
 10 15 20
 ctc atg ctg cgg aag atg gga tca aac ctg aca gcc agc gag gag gag 390
 Leu Met Leu Arg Lys Met Gly Ser Asn Leu Thr Ala Ser Glu Glu Glu
 25 30 35
 ttc ctg cgc acc tat gca ggg gtg gtc aac agc cag ctc agc cag ctg 438
 Phe Leu Arg Thr Tyr Ala Gly Val Val Asn Ser Gln Leu Ser Gln Leu
 40 45 50 55
 cct ccg cac tcc atc gac cag ggt gca gag gac gtg gtg atg gcg ttt 486
 Pro Pro His Ser Ile Asp Gln Gly Ala Glu Asp Val Val Met Ala Phe
 194/201

60	65	70	
tcc agg tcg gag acg gaa gac cgg agg cag tag ctgcaaagcc cttggaacac			539
Ser Arg Ser Glu Thr Glu Asp Arg Arg Gln			
75	80		
cctggatgct gttgaagggc caagagatct gtgtggctcc tgggccggct gaatggcagc			599
agccccctt gccccacctc ccccttcctt acccaaccct gccctgcccc accccacctc			659
acagctactc agtggggctg gcatcaaggg agacaccagt ggtgcgttta taattggctt			719
aaagggatgg acttgtgatt ggctgcagga agaaactttt ttatttttta aatcttgacc			779
aacagaaacc ttttattttt atttctgact cttatttttt aaaaaatttg cgcctcggta			839
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tgtgaagagg tctgattggc tgcttaaact ggaaagggac tgtgattggc tggttaatgg			959
gaaacggttt ttttctttgg ctgcagggtg tctgctgata tcaacagctt ccctattttg			1019
aatgcagaaa acagggtctg ggacattagt cgttatattt gacttgaaaa gaaagaaacc			1079
aagtgcgctt tgcaatatat attacacaaa gaacttgctg ctgccttcac atttgggggtt			1139
tgtgtttgat tggctttcga tgcgtgtgtt tggtttccca ttggttcacc tgtgactcct			1199
gttgccatgg attcaccccc ctctgctgcc ggctctgggc ctgagggtcc acctggagag			1259
tacatttgct ttaatgagt cacctgcctc caccagcaag gggaccccga gaaccctgag			1319
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ataaaagccc cagcttggct cacaaggccc aggagacctc cagctaaaca ccaaccctg			1739
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ggagttctct catcggaggc ccatgccctc cactccactg cctttggaag ggtctctctc			1859

caggtcagcc tggaggagac agtatcgttt gtttatgaaa tgccactggg acagctggct 1919
gggccttcac caagcaagtc ccttcagact ggcccttaag ccaaactcag gccagaatt 1979
gcagttcaga atggcagtc tggaggcagg gggtagggg caggtctagt gttcctgcac 2039
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caataaagaa ttttcatagg ttaaaaaaaaa aaaanaaaaa g 2980

<210> 73
<211> 81
<212> PRT
<213> Homo sapiens

<400> 73

Met Asn Arg Glu Gly Ala Pro Gly Lys Ser Pro Glu Glu Met Tyr Ile
1 5 10 15

Gln Gln Lys Val Arg Val Leu Leu Met Leu Arg Lys Met Gly Ser Asn
 20 25 30

Leu Thr Ala Ser Glu Glu Glu Phe Leu Arg Thr Tyr Ala Gly Val Val
 35 40 45

Asn Ser Gln Leu Ser Gln Leu Pro Pro His Ser Ile Asp Gln Gly Ala
 50 55 60

Glu Asp Val Val Met Ala Phe Ser Arg Ser Glu Thr Glu Asp Arg Arg
 65 70 75 80

Gln

<210> 74
 <211> 2153
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (589)..(1356)
 <223>

<400> 74
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 gcagaaagag cgggagctgc gactgctcat gcttggcctg gacaatgctg gaaagacaac 120
 catcctgaag aagttcaatg gggaggacat cgacaccatc tccccaacgc tgggcttcaa 180
 catcaagacc ctggagcacc gaggattcaa gctgaacatc tgggatgtgg gtggccagaa 240
 gtccctgcgg tcctactggc ggaactactt tgagagcacc gatggcctca tctgggtagt 300
 ggacagcgca gaccgccagc gcatgcagga ctgccagcgg gagctccaga gcctgctggt 360
 ggaggagtga cctgggttta cgcttcacca cagagaagga acttttcaga cgctcccttg 420
 gccgcgcacc cgggatcgga acagcgctgt cacttgcgac aaaatcccta ggccagagga 480
 agaagagcgc aggcctgggc gaggcggcgg cgggcggagg ctgggccgga ggggtgggga 540
 cggcgaggag gtggaggccg gcgctccgct ccgctccagc tcggtttc atg tcc cgc 597

Met Ser Arg

1

cag gcg aag gat gac ttc ctg cgg cac tac aca gtg tcg gac ccc agg	645
Gln Ala Lys Asp Asp Phe Leu Arg His Tyr Thr Val Ser Asp Pro Arg	
5 10 15	
act cac ccc aag ggc tac acc gag tac aaa gta acc gcg cag ttc atc	693
Thr His Pro Lys Gly Tyr Thr Glu Tyr Lys Val Thr Ala Gln Phe Ile	
20 25 30 35	
tca aag aag gac cca gag gat gtc aaa gag gtg gtg gtc tgg aag cgg	741
Ser Lys Lys Asp Pro Glu Asp Val Lys Glu Val Val Val Trp Lys Arg	
40 45 50	
tac agc gac ttc cgc aag ctg cat gga gac ctg gcc tac acc cac cgc	789
Tyr Ser Asp Phe Arg Lys Leu His Gly Asp Leu Ala Tyr Thr His Arg	
55 60 65	
aac ctc ttc cgc cgc ctc gag gag ttc cct gct ttc ccc cgg gcc cag	837
Asn Leu Phe Arg Arg Leu Glu Glu Phe Pro Ala Phe Pro Arg Ala Gln	
70 75 80	
gtg ttt ggc cgg ttt gaa gcc tca gtg atc gag gag cgg cga aag ggg	885
Val Phe Gly Arg Phe Glu Ala Ser Val Ile Glu Glu Arg Arg Lys Gly	
85 90 95	
gca gag gac ctg ctt cgc ttc act gtg cac ata cct gcg ctc aac aac	933
Ala Glu Asp Leu Leu Arg Phe Thr Val His Ile Pro Ala Leu Asn Asn	
100 105 110 115	
agc ccc cag ctc aag gag ttc ttc cgg ggt ggg gag gtg acc cga ccc	981
Ser Pro Gln Leu Lys Glu Phe Phe Arg Gly Gly Glu Val Thr Arg Pro	
120 125 130	
ttg gag gtg tcc agg gac cta cac atc ctg cca ccc cct ctg atc ccc	1029
Leu Glu Val Ser Arg Asp Leu His Ile Leu Pro Pro Pro Leu Ile Pro	
135 140 145	
acc ccg ccc cct gat gac ccc cgg cta tcc caa ctg ctc cct gca gaa	1077
Thr Pro Pro Pro Asp Asp Pro Arg Leu Ser Gln Leu Leu Pro Ala Glu	
150 155 160	
agg agg ggc ctc gag gaa ttg gag gtg cca gtg gac ccc cca cca tcc	1125
Arg Arg Gly Leu Glu Glu Leu Glu Val Pro Val Asp Pro Pro Pro Ser	
165 170 175	
agc cct gcc cag gag gcc ctg gat ctc ctc ttt aac tgt gag agc acc	1173
Ser Pro Ala Gln Glu Ala Leu Asp Leu Leu Phe Asn Cys Glu Ser Thr	
180 185 190 195	

gag gag gca tct ggt tcc cct gcc cga ggc ccc ctc acc gag gct gag	1221
Glu Glu Ala Ser Gly Ser Pro Ala Arg Gly Pro Leu Thr Glu Ala Glu	
200 205 210	
ctt gcc ctc ttc gac ccc ttc tcc aag ggt gac ccg ttg cct gcc cgc	1269
Leu Ala Leu Phe Asp Pro Phe Ser Lys Gly Asp Pro Leu Pro Ala Arg	
215 220 225	
cag gaa ggt gtg aag aag aag gca gct gag tac ctg aag cgg gca gag	1317
Gln Glu Gly Val Lys Lys Lys Ala Ala Glu Tyr Leu Lys Arg Ala Glu	
230 235 240	
gag atc ctg cgc ctg cac ctg tct caa ctc cca ccc taa cagggagtgg	1366
Glu Ile Leu Arg Leu His Leu Ser Gln Leu Pro Pro	
245 250 255	
gccattccct gggactctca ctctgcact gccagccct tctcctctcc ccagggcctg	1426
gccctacctc ctggtcttgt aattacagga gccatttctg taggtaactg gaccaagaat	1486
gagaaaaata atgaattctt agctccctga ttacacctgc caccttgga tccaggactc	1546
acacttctga ccctgcctgt ctttttgggg tttttttgag ttggagtctc gctgtgtcgc	1606
ccagactgga gtgcagtggg gggatcgagg ctactgcaa cctccacctc ccaggttcaa	1666
gcagttctcc tgtctcagcc tccccagtag ctgagattgc aggacatgc caccacgccc	1726
agctaataatt ttgtattttc agtagggacg gggttacacc atgttggcca ggctggctc	1786
gaactcctga cctcaagtga tccaccgccc tcagtctccc aaagtgctga gattacaggc	1846
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Trp Lys Arg Tyr Ser Asp Phe Arg Lys Leu His Gly Asp Leu Ala Tyr
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Thr His Arg Asn Leu Phe Arg Arg Leu Glu Glu Phe Pro Ala Phe Pro
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Arg Ala Gln Val Phe Gly Arg Phe Glu Ala Ser Val Ile Glu Glu Arg
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Arg Lys Gly Ala Glu Asp Leu Leu Arg Phe Thr Val His Ile Pro Ala
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Leu Asn Asn Ser Pro Gln Leu Lys Glu Phe Phe Arg Gly Gly Glu Val
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Thr Arg Pro Leu Glu Val Ser Arg Asp Leu His Ile Leu Pro Pro Pro
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Leu Ile Pro Thr Pro Pro Pro Asp Asp Pro Arg Leu Ser Gln Leu Leu
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Pro Ala Glu Arg Arg Gly Leu Glu Glu Leu Glu Val Pro Val Asp Pro
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Glu Ser Thr Glu Glu Ala Ser Gly Ser Pro Ala Arg Gly Pro Leu Thr
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Glu Ala Glu Leu Ala Leu Phe Asp Pro Phe Ser Lys Gly Asp Pro Leu
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Pro Ala Arg Gln Glu Gly Val Lys Lys Lys Ala Ala Glu Tyr Leu Lys
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Arg Ala Glu Glu Ile Leu Arg Leu His Leu Ser Gln Leu Pro Pro
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